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12AP1/E5 -- Viventia Biotech  
 1964 -- Aventis  
 20K growth hormone -- AMUR  
 28P6/E6 -- Viventia Biotech  
 3-Hydroxyphthaloyl-beta-lactoglobulin --  
 4-IBB ligand gene therapy --  
 64-Cu MAb conjugate TETA-1A3 --  
 Mallinckrodt Institute of Radiology  
 64-Cu MAb conjugate TETA-CT84.66  
 64-Cu Trastuzumab TETA conjugate --  
 Genentech  
 A 200 -- Amgen  
 A10255 -- Eli Lilly  
 A1PDX -- Hedral Therapeutics  
 A6 -- Angstrom  
 aaAT-III -- Genzyme  
 Abciximab -- Centocor  
 ABI.001 -- Atlantic BioPharmaceuticals  
 ABT-828 -- Abbott  
 Accutin  
 Actinohivin  
 activin -- Biotech Australia, Human  
 Therapeutics  
 activin -- Curls  
 AD 439 -- Tanox  
 AD 519 -- Tanox  
 Adalimumab -- Cambridge Antibody Tech.  
 Adenocarcinoma vaccine -- Biomira -- NIS  
 Adenosine A2B receptor antagonists --  
 Adenosine Therapeutics  
 ADP-001 -- Axis Genetics  
 AF 13948 -- Affymax  
 Afelimomab -- Knoll  
 AFP-SCAN -- Immunomedics  
 AG 2195 -- Corixa  
 agalsidase alfa -- Transkaryotic Therapies  
 agalsidase beta -- Genzyme  
 AGENT -- Antisoma  
 AI 300 -- Autolimmune  
 AI-101 -- Teva  
 AI-102 -- Teva  
 AI-201 -- Autolimmune  
 AI-301 -- Autolimmune  
 AIDS vaccine -- ANRS, CIBG, Hesed  
 Biomed, Hollis-Eden, Rome, United  
 Biomedical, American Home Products,  
 Maxygen  
 airway receptor ligand -- IC Innovations  
 AJvW 2 -- Ajinomoto  
 AK 30 NGF -- Alkermes  
 Albuferon -- Human Genome Sciences  
 albumin -- Biogen, DSM Anti-Infectives,  
 Genzyme Transgenics, PPL Therapeutics,  
 TranXenoGen, Welfide Corp.  
 aldesleukin -- Chiron  
 alefacept -- Biogen  
 Alemtuzumab --  
 Allergy therapy -- ALK-Abello/Maxygen,  
 ALK-Abello/RP Scherer  
 allergy vaccines -- Allergy Therapeutics  
 Alnidofibatide -- Aventis Pasteur  
 Alnorine -- SRC VB VECTOR  
 ALP 242 -- Gruenenthal  
 Alpha antitrypsin -- Arriva/Hyland  
 Immuno/ProMetic/Protease Sciences  
 Alpha-1 antitrypsin -- Cutter, Bayer, PPL  
 Therapeutics, Profile, ZymoGenetics,  
 Arriva  
 Alpha-1 protease inhibitor -- Genzyme  
 Transgenics, Welfide Corp.  
 Alpha-galactose fusion protein --  
 Immunomedics  
 Alpha-galactosidase A -- Research  
 Corporation Technologies  
 Alpha-glucosidase -- Genzyme, Novazyme  
 Alpha-lactalbumin  
 Alpha-L-iduronidase -- Transkaryotic  
 Therapies, BioMarin  
 alteplase -- Genentech  
 alvircept sudotox -- NIH  
 ALX1-11 -- sNPS Pharmaceuticals  
 Alzheimer's disease gene therapy --

FIG. 1A

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AM-133 -- AMRAD  
 Amb a 1 immunostim conj. -- Dynavax  
 AMD 3100 -- AnorMED -- NIS  
 AMD 3465 -- AnorMED -- NIS  
 AMD 3465 -- AnorMED -- NIS  
 AMD Fab -- Genentech  
 Amediplase -- Menarini, Novartis  
 AM-F9  
 Amoebiasis vaccine  
 Amphiregulin -- Octagene  
 anakinra -- Amgen  
 analgesic -- Nobex  
 anacstim -- Amgen  
 Anergix.RA -- Corixa, Organon  
 Angiocidin -- InKine  
 angiogenesis inhibitors -- ILEX  
 AngioMab -- Antisoma  
 Angiopoietins -- Regeneron/Procter & Gamble  
 angiostatin -- EntreMed  
 Angiostatin/endostatin gene therapy -- Genetix Pharmaceuticals  
 angiotensin-II, topical -- Maret  
 Anthrax -- EluSys Therapeutics/US Army Medical Research Institute  
 Anthrax vaccine  
 Anti platelet-derived growth factor D human monoclonal antibodies -- CuraGen  
 Anti-17-1A/ MAb 3622W94 -- GlaxoSmithKline  
 Anti-2C4 MAb -- Genentech  
 anti-4-1BB monoclonal antibodies -- Bristol-Myers Squibb  
 Anti-Adhesion Platform Tech. -- Cytovax  
 Anti-adipocyte MAb -- Cambridge Antibody Tech./Obesys  
 antiallergics -- Maxygen  
 antiallergy vaccine -- Acambis  
 Anti-alpha-4-integrin MAB  
 Anti-angiogenesis monoclonal antibodies -- KS Biomedix/Schering AG  
 Anti-B4 MAb-DC1 conjugate -- ImmunoGen  
 Anti-B7 antibody PRIMATIZED -- IDEC  
 Anti-B7-1 MAB 16-10A1  
 Anti-B7-1 MAB 1G10  
 Anti-B7-2 MAB GL-1  
 Anti-B7-2-gelonin Immunotoxin -- Antibacterials/antifungals -- Diversa/IntraBiotics  
 Anti-beta-amyloid monoclonal antibodies -- Cambridge Antibody Tech., Wyeth-Ayerst  
 Anti-BLyS antibodies -- Cambridge Antibody Tech. /Human Genome Sciences  
 Antibody-drug conjugates -- Seattle Genetics/Eos  
 Anti-C5 MAB BB5-1 -- Alexion  
 Anti-C5 MAB N19-8 -- Alexion  
 Anti-C8 MAB anticancer cytokines -- BioPulse  
 anticancer matrix -- Telios Integra  
 Anticancer monoclonal antibodies -- ARIUS, Immunex  
 anticancer peptides -- Maxygen, Micrologix  
 anticancer prodrug Tech. -- Alexion Antibody Technologies  
 anticancer Troy-Bodies -- Affite -- Affitech  
 anticancer vaccine -- NIH  
 anticancers -- Epimmune  
 Anti-CCR5/CXCR4 sheep MAB -- KS Biomedix Holdings  
 Anti-CD11a MAB KBA --  
 Anti-CD11a MAB M17  
 Anti-CD11a MAB TA-3 --  
 Anti-CD11a MAB WT.1 --  
 Anti-CD11b MAB -- Pharmacia  
 Anti-CD11b MAB LM2  
 Anti-CD154 MAB -- Biogen  
 Anti-CD16-anti-CD30 MAB -- Biotest  
 Anti-CD18 MAB -- Pharmacia  
 Anti-CD19 MAB B43 --  
 Anti-CD19 MAB -liposomal sodium butyrate conjugate --

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Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb KT6
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb OX38
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb B-E2 -- Diacalone	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX34 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb OX54 --	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-1	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD2 MAb RM2-2	Anti-CD40 MAb
Anti-CD2 MAb RM2-4	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD20 MAb BCA B20	Anti-CD44 MAb A3D8
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD44 MAb GKWA3
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb IM7
Anti-CD3 immunotoxin --	Anti-CD44 MAb KM81
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD45RB MAb
Anti-CD3 MAb WT32	Anti-CD48 MAb HuLy-m3
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD48 MAb WM-63
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30 MAb BerH2 -- Medac	Anti-CD5 MAb OX19
Anti-CD30 MAb-saporin conjugate	Anti-CD6 MAb
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD7 MAb-PAP conjugate
Anti-CD38 MAb AT13/5	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD38 MAb-saporin conjugate	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb OX8
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD80 MAb P7C10 -- ID Vaccine
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD8-idarubicin conjugate
Anti-CD4 idiotype vaccine	Anti-CEA MAb CE-25
Anti-CD4 MAb -- Centocor, IDEC Pharmaceuticals, Xenova Group	Anti-CEA MAb MN 14 -- Immunomedics
Anti-CD4 MAb 16H5	Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics
Anti-CD4 MAb 4162W94 -- GlaxoSmithKline	Anti-CEA MAb T84.66-interleukin-2 conjugate
Anti-CD4 MAb B-F5 -- Diacalone	Anti-CEA sheep MAb -- KS Biomedix Holdings
Anti-CD4 MAb GK1-5	

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- Anti-cell surface monoclonal antibodies --  
 Cambridge Antibody Tech. /Pharmacia  
 Anti-c-erbB2-anti-CD3 bifunctional MAb --  
 Otsuka  
 Anti-CMV MAb -- Scotgen  
 Anti-CTLA-4 MAb  
 Anti-EGFR catalytic antibody -- Hesed  
 Biomed  
 anti-EGFR immunotoxin -- IVAX  
 Anti-EGFR MAb -- Abgenix  
 Anti-EGFR MAb 528  
 Anti-EGFR MAb KSB 107 -- KS Biomedix  
 Anti-EGFR MAb-DM1 conjugate --  
 ImmunoGen  
 Anti-EGFR MAb-LA1 --  
 Anti-EGFR sheep MAb -- KS Biomedix  
 Anti-FAP MAb F19-I-131  
 Anti-Fas IgM MAb CH11  
 Anti-Fas MAb Jo2  
 Anti-Fas MAb RK-8  
 Anti-Flt-1 monoclonal antibodies -- ImClone  
 Anti-fungal peptides -- State University of  
 New York  
 antifungal tripeptides -- BTG  
 Anti-ganglioside GD2 antibody-interleukin-2  
 fusion protein -- Lexigen  
 Anti-GM2 MAb -- Kyowa  
 Anti-GM-CSF receptor monoclonal  
 antibodies -- AMRAD  
 Anti-gp130 MAb -- Tosoh  
 Anti-HCA monoclonal antibodies --  
 AltaRex/Epigen  
 Anti-hCG antibodies -- Abgenix/AVI  
 BioPharma  
 Anti-heparanase human monoclonal  
 antibodies -- Oxford  
 Glycosciences/Medarex  
 Anti-hepatitis C virus human monoclonal  
 antibodies -- XTL Biopharmaceuticals  
 Anti-HER-2 antibody gene therapy  
 Anti-herpes antibody -- Epicyte  
 Anti-HIV antibody -- Epicyte  
 anti-HIV catalytic antibody -- Hesed Biomed  
 anti-HIV fusion protein -- Idun  
 anti-HIV proteins -- Cangene  
 Anti-HM1-24 MAb -- Chugai  
 Anti-hR3 MAb  
 Anti-Human-Carcinoma-Antigen MAb --  
 Epicyte  
 Anti-ICAM-1 MAb -- Boehringer Ingelheim  
 Anti-ICAM-1 MAb 1A-29 -- Pharmacia  
 Anti-ICAM-1 MAb HA58  
 Anti-ICAM-1 MAb YN1/1.7.4  
 Anti-ICAM-3 MAb ICM3 -- ICOS  
 Anti-idiotypic breast cancer vaccine 11D10  
 Anti-idiotypic breast cancer vaccine  
 ACA14C5 --  
 Anti-idiotypic cancer vaccine -- ImClone  
 Systems/Merck KGaA ImClone, Viventia  
 Biotech  
 Anti-idiotypic cancer vaccine 1A7 -- Titan  
 Anti-idiotypic cancer vaccine 3H1 -- Titan  
 Anti-idiotypic cancer vaccine TriAb -- Titan  
 Anti-idiotypic Chlamydia trachomatis  
 vaccine  
 Anti-idiotypic colorectal cancer vaccine --  
 Novartis  
 Anti-idiotypic colorectal cancer vaccine --  
 Onyvax  
 Anti-idiotypic melanoma vaccine -- IDEC  
 Pharmaceuticals  
 Anti-idiotypic ovarian cancer vaccine ACA  
 125  
 Anti-idiotypic ovarian cancer vaccine AR54 -  
 - AltaRex  
 Anti-idiotypic ovarian cancer vaccine CA-  
 125 -- AltaRex, Biomira  
 Anti-IgE catalytic antibody -- Hesed Biomed  
 Anti-IgE MAb E26 -- Genentech  
 Anti-IGF-1 MAb  
 anti-inflammatory -- GeneMax  
 anti-inflammatory peptide -- BTG



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anti-integrin peptides -- Burnha	Anti-mu MAb -- Novartis
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC-1 MAb
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody -- - Dompe	Anti-nuclear autoantibodies -- Procyon
- Advanced Biotherapy	Anti-ovarian cancer monoclonal antibodies --
Anti-interleukin-10 MAb --	Anti-p185 monoclonal antibodies
Anti-interleukin-12 MAb --	Anti-p43 MAb
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Antiparasitic vaccines
Anti-interleukin-2 receptor MAB 2A3	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAB 33B3-1 -- Immunotech	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAB ART-18	Anti-PSMA MAB J591 -- BZL Biologics
Anti-interleukin-2 receptor MAB LO-Tact-1	Anti-Rev MAB gene therapy --
Anti-interleukin-2 receptor MAB Mikbeta1	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-2 receptor MAB NDS61	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-4 MAB 11B11	Anti-RSV MAB, inhalation -- Alkermes/MedImmune
Anti-interleukin-5 MAB -- Wallace Laboratories	Anti-RT gene therapy
Anti-interleukin-6 MAB -- Centocor, Diacione, Pharmadigm	Antisense K-ras RNA gene therapy
Anti-interleukin-8 MAB -- Xenotech	Anti-SF-25 MAB
Anti-JL1 MAB	Anti-sperm antibody -- Epicyte
Anti-Klebsiella sheep MAB -- KS Biomedix Holdings	Anti-Tac(Fv)-PE38 conjugate
Anti-Laminin receptor MAB-liposomal doxorubicin conjugate	Anti-TAPA/CD81 MAB AMP1
Anti-LCG MAB -- Cytoconal	Anti-tat gene therapy
Anti-lipopopolysaccharide MAB -- VitaResc	Anti-TCR-alpha-beta MAB H57-597
Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University	Anti-TCR-alpha-beta MAB R73
Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital	Anti-tenascin MAB BC-4-l-131
Anti-MHC monoclonal antibodies	Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme
Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences	Anti-TGF-beta MAB 2G7 -- Genentech
Anti-MRSA/VRSA sheep MAB -- KS Biomedix Holdings	Anti-thrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad
	Anti-Thy1 MAB
	Anti-Thy1.1 MAB

FIG. 1E

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Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix  
 Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono  
 Anti-TNF sheep MAb -- KS Biomedix Holdings  
 Anti-TNFalpha MAb -- Genzyme  
 Anti-TNFalpha MAb B-C7 -- Diaclone  
 Anti-tooth decay MAb -- Planet BioTech.  
 antitumour RNases -- NIH  
 Anti-VCAM MAb 2A2 -- Alexion  
 Anti-VCAM MAb 3F4 -- Alexion  
 Anti-VCAM-1 MAb  
 Anti-VEC MAb -- ImClone  
 Anti-VEGF MAb -- Genentech  
 Anti-VEGF MAb 2C3  
 Anti-VEGF sheep MAb -- KS Biomedix Holdings  
 Anti-VLA-4 MAb HP1/2 -- Biogen  
 Anti-VLA-4 MAb PS/2  
 Anti-VLA-4 MAb R1-2  
 Anti-VLA-4 MAb TA-2  
 Anti-VRE sheep MAb -- KS Biomedix Holdings  
 ANUP -- TranXenoGen  
 ANUP-1 -- Pharis  
 AOP-RANTES -- Senetek  
 Apan-CH -- Praecis Pharmaceuticals  
 APC-8024 -- Demegen  
 ApoA-1 -- Milano, Pharmacia  
 Apogen -- Alexion  
 apolipoprotein A1 -- Avanir  
 Apolipoprotein E -- Bio-Tech. General  
 Applaggin -- Biogen  
 aprotinin -- ProdiGene  
 APT-070C -- AdProTech  
 AR 177 -- Aronex Pharmaceuticals  
 AR 209 -- Aronex Pharmaceuticals, Antigenics  
 AR545C  
 ARGENT gene delivery systems -- ARIAD  
 Arresten  
 ART-123 -- Asahi Kasei  
 arylsulfatase B -- BioMarin  
 Arylsulfatase B, Recombinant human -- BioMarin  
 AS 1051 -- Ajinomoto  
 ASI-BCL -- Intracell  
 ATL-101 -- Alzyme  
 atrial natriuretic peptide -- Pharis  
 Aurintricarboxylic acid-high molecular weight  
 autoimmune disorders -- GPC  
 Biotech/MorphoSys  
 Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme  
 Tra  
 Autoimmune disorders/cancer -- Abgenix/Chiron, /CuraGen  
 Autotaxin  
 Avidin -- NeoRx  
 axogenesis factor-1 -- Boston Life Sciences  
 Axokine -- Regeneron  
 B cell lymphoma vaccine -- Biomira  
 B7-1 gene therapy -- BABS proteins -- Chiron  
 BAM-002 -- Novelos Therapeutics  
 Bay-16-9996 -- Bayer  
 Bay-39-9437 -- Bayer  
 Bay-50-4798 -- Bayer  
 BB-10153 -- British Biotech  
 BBT-001 -- Bolder BioTech.  
 BBT-002 -- Bolder BioTech.  
 BBT-003 -- Bolder BioTech.  
 BBT-004 -- Bolder BioTech.  
 BBT-005 -- Bolder BioTech.  
 BBT-006 -- Bolder BioTech.  
 BBT-007 -- Bolder BioTech.  
 BCH-2763 -- Shire  
 BCSF -- Millenium Biologix  
 BDNF -- Regeneron -- Amgen

FIG. 1F

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Becaplermin -- Johnson & Johnson, Chiron  
 Bectumomab -- Immunomedics  
 Beta-adrenergic receptor gene therapy --  
 University of Arkansas  
 BI 51013 -- Behringwerke AG  
 BIBH 1 -- Boehringer Ingelheim  
 BIM-23190 -- Beaufour-Ipsen  
 birch pollen immunotherapy -- Pharmacia  
 bispecific fusion proteins -- NIH  
 Bispecific Mab 2B1 -- Chiron  
 Bitistatin  
 BIWA 4 -- Boehringer Ingelheim  
 blood substitute -- Northfield, Baxter Intl.  
 BLP-25 -- Biomira  
 BLS-0597 -- Boston Life Sciences  
 BLYS -- Human Genome Sciences  
 BLYS radiolabelled -- Human Genome  
 Sciences  
 BM 06021 -- Boehringer Mannheim  
 BM-202 -- BioMarin  
 BM-301 -- BioMarin  
 BM-301 -- BioMarin  
 BM-302 -- BioMarin  
 BMP 2 -- Genetics Institute/Medtronic-  
 Sofamor Danek, Genetics Institute/  
 Collagenesis, Genetics  
 Institute/Yamanouch  
 BMP 2 gene therapy  
 BMP 52 -- Aventis Pasteur, Biopharm  
 BMP-2 -- Genetics Institute  
 BMS 182248 -- Bristol-Myers Squibb  
 BMS 202448 -- Bristol-Myers Squibb  
 bone growth factors -- IsoTis  
 BPC-15 -- Pfizer  
 brain natriuretic peptide --  
 Breast cancer -- Oxford  
 GlycoSciences/Medarex  
 Breast cancer vaccine -- Therion Biologics,  
 Oregon  
 BSSL -- PPL Therapeutics  
 BST-2001 -- BioStratum  
 BST-3002 -- BioStratum  
 BTI 322 --  
 butyrylcholinesterase -- Shire  
 C 6822 -- COR Therapeutics  
 C1 esterase inhibitor -- Pharming  
 C3d adjuvant -- AdProTech  
 CAB-2.1 -- Millennium  
 calcitonin -- Inhale Therapeutics Systems,  
 Aventis, Genetronics, TranXenoGen,  
 Unigene, Rhone Poulenc Rohrer  
 calcitonin -- oral -- Nobex, Emisphere,  
 Pharmaceutical Discovery  
 Calcitonin gene-related peptide -- Asahi  
 Kasei -- Unigene  
 calcitonin, human -- Suntory  
 calcitonin, nasal -- Novartis, Unigene  
 calcitonin, Panoderm -- Elan  
 calcitonin, Peptitol -- Shire  
 calcitonin, salmon -- Therapicon  
 calin -- Biopharm  
 Calphobindin I  
 calphobindin I -- Kowa  
 calreticulin -- NYU  
 Campath-1G  
 Campath-1M  
 cancer therapy -- Cangene  
 cancer vaccine -- Aixlie, Aventis Pasteur,  
 Center of Molecular Immunology, YM  
 BioSciences, Cytos, Genzyme,  
 Transgenics, GlobeImmune, Igeneon,  
 ImClone, Virogenetics, InterCell, Iomai,  
 Jenner Biotherapies, Memorial Sloan-  
 Kettering Cancer Center, Sydney Kimmel  
 Cancer Center, Novavax, Protein  
 Sciences, Argonex, SIGA  
 Cancer vaccine ALVAC-CEA B7.1 --  
 Aventis Pasteur/Therion Biologics  
 Cancer vaccine CEA-TRICOM -- Aventis  
 Pasteur/Therion Biologics  
 Cancer vaccine gene therapy -- Cantab  
 Pharmaceuticals

FIG. 1G

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Cancer vaccine HER-2/neu -- Corixa	CETP vaccine -- Avant
Cancer vaccine THERATOPE -- Biomira	Cetorelix
cancer vaccine, PolyMASC -- Valentis	Cetuximab
Candida vaccine -- Corixa, Inhibitex	CGH 400 -- Novartis
Canstatin -- ILEX	CGP 42934 -- Novartis
CAP-18 -- Panorama	CGP 51901 -- Tanox
Cardiovascular gene therapy -- Collateral Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase -- Enzo	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex Biologics
CB 0006 -- Celltech	Chlamydia trachomatis vaccine -- Antex Biologics
CCK(27-32) -- Akzo Nobel	Chlamydia vaccine -- GlaxoSmithKline
CCR2-641 -- NIH	Cholera vaccine CVD 103-HgR -- Swiss Serum and Vaccine Institute Berne
CD, Procept -- Paligent	Cholera vaccine CVD 112 -- Swiss Serum and Vaccine Institute Berne
CD154 gene therapy	Cholera vaccine inactivated oral -- SBL Vaccin
CD39 -- Immunex	Chrysalin -- Chrysalis BioTech.
CD39-L2 -- Hyseq	CI-782 -- Hitachi Kase
CD39-L4 -- Hyseq	Ciliary neurotrophic factor -- Fidia, Roche
CD4 fusion toxin -- Senetek	CIM project -- Active Biotech
CD4 IgG -- Genentech	CL 329753 -- Wyeth-Ayerst
CD4 receptor antagonists -- Pharmacopeia/Progenics	CL22, Cobra -- ML Laboratories
CD4 soluble -- Progenics	Clenoliximab -- IDEC
CD4, soluble -- Genzyme Transgenics	Clostridium difficile antibodies -- Epicyte
CD40 ligand -- Immunex	clotting factors -- Octagene
CD4-ricin chain A -- Genentech	CMB 401 -- Celltech
CD59 gene therapy -- Alexion	CNTF -- Sigma-Tau
CD8 TIL cell therapy -- Aventis Pasteur	Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps
CD8, soluble -- Avidex	coccidiomycosis vaccine -- Arizo
CD95 ligand -- Roche	collagen -- Type I -- Pharming
CDP 571 -- Celltech	Collagen formation inhibitors -- FibroGen
CDP 850 -- Celltech	
CDP 870 -- Celltech	
CDS-1 -- Ernest Orlando	
Cedelizumab -- Ortho-McNeil	
Cetermin -- Insmed	

FIG. 1H

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Collagen/hydroxyapatite/bone growth factor	CY 1747 -- Epimmune
-- Aventis Pasteur, Biopharm, Orquest	CY 1748 -- Epimmune
collagenase -- BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine -- Wistar Institute	Cystic fibrosis therapy -- CBR/IVAX
Component B, Recombinant -- Serono	CYT 351
Connective tissue growth factor inhibitors --	cytokine Traps -- Regeneron
FibroGen/Taisho	cytokines -- Enzon, Cytoconal
Contortrostatin	Cytomegalovirus glycoprotein vaccine --
contraceptive vaccine -- Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible --	Cytomegalovirus vaccine live -- Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida --	Cytosine deaminase gene therapy --
Zonagen	GlaxoSmithKline
Copper-64 labelled MAb TETA-1A3 -- NCI	DA-3003 -- Dong-A
Coralyne	DAB389interleukin-6 -- Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues -- Schwarz	DAMP <sup>A</sup> -- Incyte Genomics
CPI-1500 -- Consensus	Daniplestim -- Pharmacia
CRF -- Neurobiological Tech.	darbepoetin alfa -- Amgen
cRGDFV pentapeptide --	DBI-3019 -- Diabetogen
CRL 1095 -- CytRx	DCC -- Genzyme
CRL 1336 -- CytRx	DDF -- Hyseq
CRL 1605 -- CytRx	decorin -- Integra, Telios
CS-560 -- Sankyo	defensins -- Large Scale Biology
CSF -- ZymoGenetics	DEGR-VIIa
CSF-G -- Hangzhou, Dong-A, Hanmi	Delimmunised antibody 3B6/22 AGEN
CSF-GM -- Cangene, Hunan, LG Chem	Deimmunised anti-cancer antibodies --
CSF-M -- Zarix	Biovation/Viragen
CT 1579 -- Merck Frosst	Dendroamide A
CT 1786 -- Merck Frosst	Dengue vaccine -- Bavarian Nordic, Merck
CT-112 <sup>A</sup> -- BTG	denileukin diftitox -- Ligand
CTB-134L -- Xenova	DES-1101 -- Desmos
CTC-111 -- Kaketsuken	desirudin -- Novartis
CTGF -- FibroGen	desmopressin -- Unigene
CTLA4-Ig -- Bristol-Myers Squibb	Desmoteplase -- Merck, Schering AG
CTLA4-Ig gene therapy --	Destabilase
CTP-37 -- AVI BioPharma	Diabetes gene therapy -- DeveloGen, Pfizer
C-type natriuretic peptide -- Suntory	Diabetes therapy -- Crucell
CVS 995 -- Corvas Int'l.	Diabetes type 1 vaccine -- Diamyd
CX 397 -- Nikko Kyodo	Therapeutics

FIG. 11

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DiaCIM -- YM BioSciences  
 dialytic oligopeptides -- Research Corp  
 Diamyd -- Diamyd Therapeutics  
 DiaPep227 -- Pepgen  
 DiavaX -- Corixa  
 Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline  
 DIR therapy -- Solis Therapeutics --  
 DNase -- Genentech  
 Dornase alfa -- Genentech  
 Dornase alfa, inhalation -- Genentech  
 Doxorubicin-anti-CEA MAb conjugate -- Immunomedics  
 DP-107 -- Trimeris  
 drotrecogin alfa -- Eli Lilly  
 DTctGMCSF  
 DTP-polio vaccine -- Aventis Pasteur  
 DU 257-KM231 antibody conjugate -- Kyowa  
 dural graft matrix -- Integra  
 Duteplase -- Baxter Intl.  
 DWP-401 -- Daewoong  
 DWP-404 -- Daewoong  
 DWP-408 -- Daewoong  
 E coli O157 vaccine -- NIH  
 E21-R -- BresaGen  
 Eastern equine encephalitis virus vaccine --  
 Echicetin --  
 Echinhibin 1 --  
 Echistatin -- Merck  
 Echitamine --  
 EC-SOD -- PPL Therapeutics  
 EDF -- Ajinomoto  
 EDN derivative -- NIH  
 EDNA -- NIH  
 Edobacomab -- XOMA  
 Edrecolomab -- Centocor  
 EF 5077  
 Efalizumab -- Genentech  
 EGF fusion toxin -- Seragen, Ligand  
 EGF-P64k vaccine -- Center of Molecular Immunology  
 EL 246 -- LigoCyte  
 elastase inhibitor -- Synergen  
 elcatonin -- Therapicon  
 EMD 72000 -- Merck KGaA  
 Emdogain -- BIORA  
 emfillermin -- AMRAD  
 Emoctakin -- Novartis  
 enamel matrix protein -- BIORA  
 Endo III -- NYU  
 endostatin -- EntreMed, Pharis  
 Enhancins -- Micrologix  
 Enlimomab -- Isis Pharm.  
 Enoxaparin sodium -- Pharmuka  
 enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings  
 Eosinophil-derived neutralizing agent --  
 EP-51216 -- Asta Medica  
 EP-51389 -- Asta Medica  
 EPH family ligands -- Regeneron  
 Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson  
 Epidermal growth factor fusion toxin -- Senetek  
 Epidermal growth factor-genistein --  
 EPI-HNE-4 -- Dyax  
 EPI-KAL2 -- Dyax  
 Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin  
 Epratuzumab -- Immunomedics  
 Epstein-Barr virus vaccine --  
 Aviron/SmithKline Beecham, Bioresearch  
 Eptacog alfa -- Novo Nordisk  
 Eptifibatide -- COR Therapeutics  
 erb-38 --  
 Erlizumab -- Genentech

FIG. 1J

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erythropoietin -- Alkermes, ProLease, Dong-Fas TR -- Human Genome Sciences  
 A, Elanex, Genetics Institute, LG Chem,  
 Protein Sciences, Serono, Snow Brand,  
 SRC VB VECTOR, Transkaryotic  
 Therapies  
 Erythropoietin Beta -- Hoffman La Roche  
 Erythropoietin/Epoetin alfa -- Chugai  
 Escherichia coli vaccine -- North American  
 Vaccine, SBL Vaccin, Swiss Serum and  
 Vaccine Institute Berne  
 etanercept -- Immunex  
 examorelin -- Mediolanum  
 exonuclease VII  
 F 105 -- Centocor  
 F-992 -- Fornix  
 Factor IX -- Alpha Therapeutics, Welfide  
 Corp., CSL, enetics Institute/AHP,  
 Pharmacia, PPL Therapeutics  
 Factor IX gene therapy -- Cell Genesys  
 Factor VII -- Novo Nordisk, Bayer, Baxter  
 Intl.  
 Factor VIIa -- PPL Therapeutics,  
 ZymoGenetics  
 Factor VIII -- Bayer Genentech, Beaufour-  
 Ipsen, CLB, Inex, Octagen, Pharmacia,  
 Pharming  
 Factor VIII -- PEGylated -- Bayer  
 Factor VIII fragments -- Pharmacia  
 Factor VIII gene therapy -- Targeted  
 Genetics  
 Factor VIII sucrose formulation -- Bayer,  
 Genentech  
 Factor VIII-2 -- Bayer  
 Factor VIII-3 -- Bayer  
 Factor Xa inhibitors -- Merck, Novo Nordisk,  
 Mochida  
 Factor XIII -- ZymoGenetics  
 Factors VIII and IX gene therapy -- Genetics  
 Institute/Targeted Genetics  
 Famoxin -- Genset  
 Fas (delta) TM protein -- LXR BioTech.  
 Felvizumab -- Scotgen  
 FFR-VIIa -- Novo Nordisk  
 FG-001 -- F-Gene  
 FG-002 -- F-Gene  
 FG-004 -- F-Gene  
 FG-005 -- F-Gene  
 FGF + fibrin -- Repair  
 Fibrimage -- Bio-Tech. General  
 fibrin-binding peptides -- ISIS Innovation  
 fibrinogen -- PPL Therapeutics, Pharming  
 fibroblast growth factor -- Chiron, NYU,  
 Ramot, ZymoGenetics  
 fibrolase conjugate -- Schering AG  
 Filgrastim -- Amgen  
 filgrastim -- PDA modified -- Xencor  
 FLT-3 ligand -- Immunex  
 FN18 CRM9 --  
 follistatin -- Biotech Australia, Human  
 Therapeutics  
 follitropin alfa -- Alkermes, ProLease,  
 PowderJect, Serono, Akzo Nobel  
 Follitropin Beta -- Bayer, Organon  
 FP 59  
 FSH -- Ferring  
 FSH + LH -- Ferring  
 F-spondin -- CeNeS  
 fusion protein delivery system -- UAB  
 Research Foundation  
 fusion toxins -- Boston Life Sciences  
 G 5598 -- Genentech  
 GA-II -- Transkaryotic Therapies  
 Gamma-interferon analogues -- SRC VB  
 VECTOR  
 Ganirelix -- Roche  
 gastric lipase -- Meristem  
 Gavilimomab --  
 G-CSF -- Amgen, SRC VB VECTOR  
 GDF-1 -- CeNeS  
 GDF-5 -- Biopharm  
 GDNF -- Amgen

FIG. 1K

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gelsolin -- Biogen  
 Gemtuzumab ozogamicin -- Celltech  
 Gene-activated epoetin-alfa -- Aventis  
 Pharma -- Transkaryotic Therapies  
 Glanzmann thrombasthenia gene therapy --  
 Glatiramer acetate -- Yeda  
 glial growth factor 2 -- CeNeS  
 GLP-1 -- Amylin, Suntory, TheraTech,  
 Watson  
 GLP-1 peptide analogues -- Zealand  
 Pharmaceuticals  
 glucagon -- Eli Lilly, ZymoGenetics  
 Glucagon-like peptide-1 7-36 amide --  
 Suntory  
 Glucocerebrosidase -- Genzyme  
 glutamate decarboxylase -- Genzyme  
 Transgenics  
 Glycoprotein S3 -- Kureha  
 GM-CSF -- Immunex  
 GM-CSF tumour vaccine -- PowderJect  
 GnRH immunotherapeutic -- Protherics  
 gp75 antigen -- ImClone  
 gp96 -- Antigenics  
 GPI 0100 -- Galenica  
 GR 4991W93 -- GlaxoSmithKline  
 Granulocyte colony-stimulating factor --  
 Dong-A  
 Granulocyte colony-stimulating factor  
 conjugate  
 grass allergy therapy -- Dynavax  
 GRF1-44 -- ICN  
 Growth Factor -- Chiron, Atrigel, Atrix,  
 Innogenetics, ZymoGenetics, Novo  
 growth factor peptides -- Biotherapeutics  
 growth hormone -- LG Chem  
 growth hormone, Recombinant human --  
 SeroNo  
 GT 4086 -- Gliatech  
 GW 353430 -- GlaxoSmithKline  
 GW-278884 -- GlaxoSmithKline  
 H 11 -- Viventia Biotech  
 H5N1 influenza A virus vaccine -- Protein  
 Sciences  
 haemoglobin -- Biopure  
 haemoglobin 3011, Recombinant -- Baxter  
 Healthcare  
 haemoglobin crosfumaril -- Baxter Intl.  
 haemoglobin stabilized -- Ajinomoto  
 haemoglobin, recombinant -- Apex  
 HAF -- Immune Response  
 Hantavirus vaccine  
 HB 19  
 HBNF -- Regeneron  
 HCC-1 -- Pharis  
 hCG -- Milkhaus  
 hCG vaccine -- Zonagen  
 HE-317 -- Hollis-Eden Pharmaceuticals  
 Heat shock protein cancer and influenza  
 vaccines -- StressGen  
 Helicobacter pylori vaccine -- Acambis,  
 AstraZeneca/CSL, Chiron, Provalis  
 Helistat-G -- GalaGen  
 Hemolink -- Hemosol  
 hepapoietin -- Snow Brand  
 heparanase -- InSight  
 heparinase I -- Ibex  
 heparinase III -- Ibex  
 Hepatitis A vaccine -- American Biogenetic  
 Sciences  
 Hepatitis A vaccine inactivated  
 Hepatitis A vaccine Nothav -- Chiron  
 Hepatitis A-hepatitis B vaccine --  
 GlaxoSmithKline  
 hepatitis B therapy -- Tripep  
 Hepatitis B vaccine -- Amgen, Chiron SpA,  
 Meiji Milk, NIS, Prodeva, PowderJect,  
 Rhein Biotech  
 Hepatitis B vaccine recombinant -- Evans  
 Vaccines, Epitex Combiotech, Genentech,  
 MedImmune, Merck Sharp & Dohme,  
 Rhein Biotech, Shantha Biotechnics,  
 Vector, Yeda

FIG. 1L



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- Hepatitis B vaccine recombinant TGP 943 -- HIV peptides -- American Home Products  
Takeda  
HIV vaccine -- Applied bioTech., Axis  
Genetics, Biogen, Bristol-Myers Squibb,  
Genentech, Korea Green Cross, NIS,  
Oncogen, Protein Sciences Corporation,  
Terumo, Tonen Corporation, Wyeth-  
Ayerst, Wyeth-Lederle Vaccines-Malvern,  
Advanced BioScience Laboratories,  
Bavarian Nordic, Bavarian Nordic/Statens  
Serum Institute, GeneCure, Immune  
Response, Progenics, Theron Biologics,  
United Biomedical, Chiron
- Hepatitis C vaccine -- Bavarian Nordic,  
Chiron, Innogenetics Acambis,  
Hepatitis D vaccine -- Chiron Vaccines  
Hepatitis E vaccine recombinant --  
Genelabs/GlaxoSmithKline, Novavax  
hepatocyte growth factor -- Panorama,  
Sosei  
hepatocyte growth factor kringle fragments -  
- EntrelMed  
Her-2/Neu peptides -- Corixa  
Herpes simplex glycoprotein DNA vaccine -- HIV vaccine vCP1433 -- Aventis Pasteur  
Merck, Wyeth-Lederle Vaccines-Malvern,  
Genentech, GlaxoSmithKline, Chiron,  
Takeda  
HIV vaccine vCP1452 -- Aventis Pasteur  
HIV vaccine vCP205 -- Aventis Pasteur  
HL-9 -- American BioScience  
HM-9239 -- Cytran  
HML-103 -- Hemosol  
HML-104 -- Hemosol  
HML-105 -- Hemosol  
HML-109 -- Hemosol  
HML-110 -- Hemosol  
HML-121 -- Hemosol  
hNLP -- Pharis  
Hookworm vaccine  
host-vector vaccines -- Henogen
- Herpes simplex vaccine -- Cantab  
Pharmaceuticals, CEL-SCI, Henderson  
Morley  
Herpes simplex vaccine live -- ImClone  
Systems/Wyeth-Lederle, Aventis Pasteur  
HGF derivatives -- Dompe  
hiAPP vaccine -- Crucell  
Hib-hepatitis B vaccine -- Aventis Pasteur  
HIC 1  
HIP -- Altachem  
Hirudins -- Biopharma, Cangene, Dongkook,  
Japan Energy Corporation, Pharmacia  
Corporation, SIR International, Sanofi-  
Synthelabo, Sotragene, Rhein Biotech  
HIV edible vaccine -- ProdiGene  
HIV gp120 vaccine -- Chiron, Ajinomoto,  
GlaxoSmithKline, ID Vaccine, Progenics,  
VaxGen  
HIV gp120 vaccine gene therapy --  
HIV gp160 DNA vaccine -- PowderJect,  
Aventis Pasteur, Oncogen, Hyland  
Immuno, Protein Sciences  
HIV gp41 vaccine -- Panacos  
HIV HGP-30W vaccine -- CEL-SCI  
HIV immune globulin -- Abbott, Chiron
- HPM 1 -- Chugai  
HPV vaccine -- MediGene  
HSA -- Meristem  
HSF -- StressGen  
HSP carriers -- Weizmann, Yeda, Peptor  
HSPPC-70 -- Antigenics  
HSPPC-96 -- pathogen-derived --  
Antigenics  
HSV 863 -- Novartis  
HTLV-I DNA vaccine  
HTLV-I vaccine  
HTLV-II vaccine -- Access  
HU 901 -- Tanox  
Hu23F2G -- ICOS  
HuHMF61

FIG. 1M

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HumaLYM -- Intracell	HuMax-IL15 -- Genmab
Human krebs statika -- Yamanouchi	HYB 190 -- Hybridon
human monoclonal antibodies --	HYB 676 -- Hybridon
Abgenix/Biogen, Abgenix/ Corixa,	I-125 Mab A33 -- Celltech
Abgenix/ImmuneX, Abgenix/Lexicon,	Ibritumomab tiuxetan -- IDEC
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9401 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IBT-9402 -- Ibex
Centocor/Medarex, Corixa/Kirin Brewery,	IC 14 -- ICOS
Corixa/Medarex, Eos BioTech./Medarex,	Idarubicin anti-Ly-2.1 --
Eos/Xenerex, Exelixis/Protein Design	IDEC 114 -- IDEC
Labs, ImmunoGen/ Raven,	IDEC 131 -- IDEC
Medarex/B.Twelve,	IDEC 152 -- IDEC
MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals
Human monoclonal antibodies --	iduronate-2-sulfatase -- Transkaryotic
Medarex/Northwest Biotherapeutics,	Therapies
Medarex/Seattle Genetics	IGF/IBP-2-13 -- Pharis
human netrin-1 -- Exelixis	IGN-101 -- Igeneon
human papillomavirus antibodies -- Epicyte	IK HIR02 -- Iketon
Human papillomavirus vaccine -- Biotech	IL-11 -- Genetics Institute/AHP
Australia, IDEC, StressGen	IL-13-PE38 -- NeoPharm
Human papillomavirus vaccine MEDI 501 --	IL-17 receptor -- ImmuneX
MedImmune/GlaxoSmithKline	IL-18BP -- Yeda
Human papillomavirus vaccine MEDI	IL-1Hy1 -- Hyseq
503/MEDI 504 --	IL-1B -- Celltech
MedImmune/GlaxoSmithKline	IL-1B adjuvant -- Celltech
Human papillomavirus vaccine TA-CIN --	IL-2 -- Chiron
Cantab Pharmaceuticals	IL-2 + IL-12 -- Hoffman La-Roche
Human papillomavirus vaccine TA-HPV --	IL-6/sIL-6R fusion -- Hadasit
Cantab Pharmaceuticals	IL-6R derivative -- Tosoh
Human papillomavirus vaccine TH-GW --	IL-7-Dap 389 fusion toxin -- Ligand
Cantab/GlaxoSmithKline	IM-862 -- Cytran
human polyclonal antibodies -- Biosite/Eos	IMC-1C11 -- ImClone
BioTech./ Medarex	imiglucerase -- Genzyme
human type II anti factor VIII monoclonal	Immune globulin intravenous (human) --
antibodies -- ThromboGenics	Hoffman La Roche
humanised anti glycoprotein Ib murine	immune privilege factor -- Proneuron
monoclonal antibodies -- ThromboGenics	Immunocal -- Immunotec
HumaRAD -- Intracell	Immunogene therapy -- Briana Bio-Tech
HuMax EGFR -- Genmab	Immunoliposomal 5-fluorodeoxyuridine-
HuMax-CD4 -- Medarex	dipalmitate --

FIG. 1N

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immunosuppressant vaccine -- Aixlie  
 immunotoxin -- Antisoma, NIH  
 ImmuRAIT-Re-188 -- Immunomedics  
 imreg-1 -- Imreg  
 infertility -- Johnson & Johnson, E-TRANS  
 Influenza virus vaccine -- Aventis Pasteur,  
 Protein Sciences  
 inhibin -- Biotech Australia, Human  
 Therapeutics  
 Inhibitory G protein gene therapy  
 INKP-2001 -- InKine  
 Inolimomab -- Diaclone  
 insulin -- AutoImmune, Altea, Biobras,  
 BioSante, Bio-Tech. General, Chong Kun  
 Dang, Emisphere, Flamel, Provalis, Rhein  
 Biotech, TranXenoGen  
 insulin (bovine) -- Novartis  
 insulin analogue -- Eli Lilly  
 Insulin Aspart -- Novo Nordisk  
 insulin detemir -- Novo Nordisk  
 insulin glargine -- Aventis  
 insulin inhaled -- Inhale Therapeutics  
 Systems, Alkermes  
 insulin oral -- Inovax  
 insulin, AeroDose -- AeroGen  
 insulin, AERx -- Aradigm  
 insulin, BEODAS -- Elan  
 insulin, Biphax -- Helix  
 insulin, buccal -- Generex  
 insulin, i2R -- Flemington  
 insulin, intranasal -- Bentley  
 insulin, oral -- Nobex, Unigene  
 insulin, Orasome -- Endorex  
 insulin, ProMaxx -- Epic  
 insulin, Quadrant -- Elan  
 insulin, recombinant -- Aventis  
 insulin, Spiros -- Elan  
 insulin, Transfersome -- IDEA  
 insulin, Zymo, recombinant -- Novo Nordisk  
 insulinotropin -- Scios  
 Insulysin gene therapy --  
 integrin antagonists -- Merck  
 Interferon (Alpha2) -- SRC VB VECTOR,  
 Viragen, Dong-A, Hoffman La-Roche,  
 Genentech  
 Interferon -- BioMedicines, Human Genome  
 Sciences  
 Interferon (Alfa-n3) -- Interferon Sciences  
 Intl.  
 Interferon (Alpha), Biphax -- Helix  
 Interferon (Alpha) -- Amgen, BioNative,  
 Novartis, Genzyme Transgenics,  
 Hayashibara, Inhale Therapeutics  
 Systems, Medusa, Flamel, Dong-A,  
 GeneTrol, Nastech, Shantha,  
 Wassermann, LG Chem, Sumitomo,  
 Aventis, Behring EGIS, Pepgen, Servier,  
 Rhein Biotech,  
 Interferon (Alpha2A)  
 Interferon (Alpha2B) -- Enzon, Schering-  
 Plough, Biogen, IDEA  
 Interferon (Alpha-N1) -- GlaxoSmithKline  
 Interferon (beta) -- Rentschler, GeneTrol,  
 Meristem, Rhein Biotech, Toray, Yeda,  
 Daiichi, Mochida  
 Interferon (Beta1A) -- Serono, Biogen  
 Interferon (beta1A), Inhale -- Biogen  
 Interferon (B1b) -- Chiron  
 Interferon (tau) -- Pepgen  
 Interferon alfacon-1 -- Amgen  
 Interferon alpha-2a vaccine  
 Interferon Beta 1b -- Schering/Chiron,  
 InterMune  
 Interferon Gamma -- Boehringer Ingelheim,  
 Sheffield, Rentschler, Hayashibara  
 Interferon receptor, Type I -- Serono  
 Interferon (Gamma1B) -- Genentech  
 Interferon-alpha-2b + ribavirin -- Biogen,  
 ICN  
 Interferon-alpha-2b gene therapy --  
 Schering-Plough  
 Interferon-con1 gene therapy --

FIG. 10

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interleukin-1 antagonists -- Dompe  
 Interleukin-1 receptor antagonist -- Abbott  
     Bloersearch, Pharmacia  
 Interleukin-1 receptor type I -- Immunex  
 interleukin-1 receptor Type II -- Immunex  
 Interleukin-10 -- DNAX, Schering-Plough  
 Interleukin-10 gene therapy --  
 interleukin-12 -- Genetics Institute, Hoffman  
     La-Roche  
 interleukin-13 -- Sanofi  
 Interleukin-13 antagonists -- AMRAD  
 Interleukin-13-PE38QQR  
 interleukin-15 -- Immunex  
 interleukin-16 -- Research Corp  
 interleukin-18 -- GlaxoSmithKline  
 Interleukin-1-alpha -- Immunex/Roche  
 interleukin-2 -- SRC VB VECTOR,  
     Ajinomoto, Biomira  
 Interleukin-3 -- Cangene  
 Interleukin-4 -- Immunology Ventures,  
     Sanofi Winthrop, Schering-Plough,  
     Immunex/ Sanofi Winthrop, Bayer, Ono  
 Interleukin-4 + TNF-Alpha -- NIH  
 interleukin-4 agonist -- Bayer  
 interleukin-4 fusion toxin -- Ligand  
 Interleukin-4 receptor -- Immunex, Immun  
 Interleukin-6 -- Ajinomoto, Cangene, Yeda,  
     Genetics Institute, Novartis  
 interleukin-6 fusion protein --  
 interleukin-6 fusion toxin -- Ligand, Sero  
 Interleukin-7 -- IC Innovations  
 interleukin-7 receptor -- Immunex  
 interleukin-8 antagonists -- Kyowa  
     Hakko/Millennium/Pfizer  
 interleukin-9 antagonists -- Genaera  
 interleukins -- Cel-Sci  
 Iodine I 131 tositumomab -- Corixa  
 Ior EPOCIM -- Center of Molecular  
     Immunology  
 Ior-P3 -- Center of Molecular Immunology  
 IP-10 -- NIH  
 IPF -- Metabolex  
 IR-501 -- Immune Response  
 ISIS 9125 -- Isis Pharmaceuticals  
 ISURF No. 1554 -- Millennium  
 ISURF No. 1866 -- Iowa State Univer.  
 ITF-1697 -- Italfarmaco  
 IxC 162 -- Ixion  
 J 695 -- Cambridge Antibody Tech.,  
     Genetics Inst., Knoll  
 Jagged + FGF -- Repair  
 JKC-362 -- Phoenix Pharmaceuticals  
 JTP-2942 -- Japan Tobacco  
 Juman monoclonal antibodies --  
     Medarex/Raven  
 K02 -- Axs Pharmaceuticals  
 Keliximab -- IDEC  
 Keyhole limpet haemocyanin  
 KGF -- Amgen  
 KM 871 -- Kyowa  
 KPI 135 -- Scios  
 KPI-022 -- Scios  
 Kringle 5  
 KSB 304  
 KSB-201 -- KS Biomedix  
 L 696418 -- Merck  
 L 703801 -- Merck  
 L1 -- Acorda  
 L-761191 -- Merck  
 lactoferrin -- Meristem, Pharming, Agennix  
 lactoferrin cardio -- Pharming  
 LAG-3 -- Sero  
 LAIT -- GEMMA  
 LAK cell cytotoxin -- Arizona  
 lamellarins -- PharmaMar/University of  
     Malaga  
 laminin A peptides -- NIH  
 lanoteplase -- Genetics Institute  
 Iaronidase -- BioMarin  
 Lassa fever vaccine  
 LCAT -- NIH  
 LDP 01 -- Millennium

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LDP 02 -- Millennium  
 Lecithinized superoxide dismutase --  
 Seikagaku  
 LeIF adjuvant -- Corixa  
 leishmaniasis vaccine -- Corixa  
 lenercept -- Hoffman La-Roche  
 Lenograstim -- Aventis, Chugai  
 lepirudin -- Aventis  
 leptin -- Amgen, IC Innovations  
 Leptin gene therapy -- Chiron Corporation  
 leptin, 2nd-generation -- Amgen  
 leridistim -- Pharmacia  
 leuprolide, ProMaxx -- Epic  
 leuprorelin, oral -- Unigene  
 LeuTech -- Papatin  
 LEX 032 -- SuperGen  
 LiDEPT -- Novartis  
 lipase -- Altus Biologics  
 lipid A vaccine -- EntreMed  
 lipid-linked anchor Tech. -- ICRT, ID  
 Biomedical  
 liposome-CD4 Tech. -- Sheffield  
 Listeria monocytogenes vaccine  
 LMB 1  
 LMB 7  
 LMB 9 -- Battelle Memorial Institute, NIH  
 LM-CD45 -- Cantab Pharmaceuticals  
 lovastatin -- Merck  
 LSA-3  
 LT- $\beta$  receptor -- Biogen  
 lung cancer vaccine -- Corixa  
 lusupultide -- Scios  
 L-Vax -- AVAX  
 LY 355455 -- Eli Lilly  
 LY 366405 -- Eli Lilly  
 LY-355101 -- Eli Lilly  
 Lyme disease DNA vaccine -- Vical/Aventis  
 Pasteur  
 Lyme disease vaccine -- Aquila  
 Biopharmaceuticals, Aventis, Pasteur,  
 Symbicom, GlaxoSmithKline, Hyland  
 Immuno, MedImmune  
 Lymphocytic choriomeningitis virus vaccine  
 lymphoma vaccine -- Biomira, Genitope  
 LYP18  
 lys plasminogen, recombinant  
 Lysosomal storage disease gene therapy --  
 Avigen  
 lysostaphin -- Nutrition 21  
 M 23 -- Gruenenthal  
 M1 monoclonal antibodies -- Acorda  
 Therapeutics  
 MA 16N7C2 -- Corvas Intl.  
 malaria vaccine -- GlaxoSmithKline,  
 AdProTech, Antigenics, Apovia, Aventis  
 Pasteur, Axis Genetics, Behringwerke,  
 CDCP, Chiron Vaccines, Genzyme  
 Transgenics, Hawaii, MedImmune, NIH,  
 NYU, Oxon, Roche/Saramane, Biotech  
 Australia, Rx Tech  
 Malaria vaccine CDC/NIIMALVAC-1  
 malaria vaccine, multicomponent  
 mammaglobin -- Corixa  
 mammastatin -- Biotherapeutics  
 mannan-binding lectin -- Natlmmu  
 mannan-MUC1 -- Psiron  
 MAP 30  
 Marinovir -- Phytera  
 MARstem -- Maret  
 MB-015 -- Mochida  
 MBP -- ImmuLogic  
 MCI-028 -- Mitsubishi-Tokyo  
 MCF -- Human Genome Sciences  
 MDC -- Advanced BioScience -- Akzo  
 Nobel, ICOS  
 MDX 11 -- Medarex  
 MDX 210 -- Medarex  
 MDX 22 -- Medarex  
 MDX 22

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MDX 240 -- Medarex	Methionine lyase gene therapy --
MDX 33	AntiCancer
MDX 44 -- Medarex	Met-RANTES -- Genexa Biomedical,
MDX 447 -- Medarex	Serono
MDX H210 -- Medarex	Metreleptin
MDX RA -- Houston BioTech., Medarex	MGDF -- Kirin
ME-104 -- Pharmexa	MGV -- Progenics
Measles vaccine	micrin -- Endocrine
Mecasmerin -- Cephalon/Chiron, Chiron	microplasmin -- ThromboGenics
MEDI 488 -- MedImmune	MIF -- Genetics Institute
MEDI 500	migration inhibitory factor -- NIH
MEDI 507 -- BioTransplant	Mim CD4.1 -- Xyte Therapies
melanin concentrating hormone --	mirostipen -- Human Genome Sciences
Neurocrine Biosciences	MK 852 -- Merck
melanocortins -- OMRF	Mobenakin -- NIS
Melanoma monoclonal antibodies -- Viragen	molgramostim -- Genetics Institute, Novartis
melanoma vaccine -- GlaxoSmithKline,	monoclonal antibodies -- Abgenix/Celltech,
Akzo Nobel, Avant, Aventis Pasteur,	Immusol/ Medarex, Viragen/ Roslin
Bavarian Nordic, Biovector, CancerVax,	Institute, Cambridge Antibody Tech./Elan
Genzyme Molecular Oncology, Humbolt,	MAb 108 --
ImClone Systems, Memorial, NYU, Oxxon	MAb 10D5 --
Melanoma vaccine Magevac -- Therion	MAb 14.18-interleukin-2 immunocytokine --
memory enhancers -- Scios	Lexigen
meningococcal B vaccine -- Chiron	MAb 14G2a --
meningococcal vaccine -- CAMR	MAb 15A10 --
Meningococcal vaccine group B conjugate -	MAb 170 -- Biomira
- North American Vaccine	MAb 177Lu CC49 --
Meningococcal vaccine group B	MAb 17F9
recombinant -- BioChem Vaccines,	MAb 1D7
Microscience	MAb 1F7 -- Immune Network
Meningococcal vaccine group Y conjugate -	MAb 1H10-doxorubicin conjugate
- North American Vaccine	MAb 26-2F
Meningococcal vaccine groups A B and C	MAb 2A11
conjugate -- North American Vaccine	MAb 2E1 -- RW Johnson
Mepolizumab -- GlaxoSmithKline	MAb 2F5
Metastatin -- EntreMed, Takeda	MAb 31.1 -- International BiImmune
Met-CkB7 -- Human Genome Sciences	Systems
met-enkephalin -- TNI	MAb 32 -- Cambridge Antibody Tech.,
METH-1 -- Human Genome Sciences	Peptech
methioninase -- AntiCancer	MAb 323A3 -- Centocor
	MAb 3C5

FIG. 1R

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MAb 3F12	MAb C242-PE conjugate
MAb 3F8	MAB c30-6
MAb 42/6	MAB CA208-cytorhodin-S conjugate --
MAb 425 -- Merck KGaA	Hoechst Japan
MAb 447-52D -- Merck Sharp & Dohme	MAB CC49 -- Enzon
MAb 45-2D9- -- haematoporphyrin	MAB ch14.18 --
conjugate	MAB CH14.18-GM-CSF fusion protein --
MAB 4B4	Lexigen
MAB 4E3-CPA conjugate -- BCM Oncologia	MAB chCE7
MAB 4E3-daunorubicin conjugate	MAB CI-137 -- AMRAD
MAB 50-6	MAB cisplatin conjugate
MAB 50-61A -- Institut Pasteur	MAB CLB-CD19
MAB 5A8 -- Biogen	MAB CLB-CD19v
MAB 791T/36-methotrexate conjugate	MAB CLL-1 -- Peregrine
MAB 7c11.e8	MAB CLL-1-GM-CSF conjugate
MAB 7E11 C5-selenocystamine conjugate	MAB CLL-1-IL-2 conjugate -- Peregrine
MAB 93KA9 -- Novartis	MAB CLN IgG -- doxorubicin conjugates
MAB A5B7-cisplatin conjugate --	MAB conjugates -- Tanox
Biodynamics Research, Pharmacia	MAB D612
MAB A5B7-I-131	MAB Dal B02
MAB A7	MAB DC101 -- ImClone
MAB A717 -- Exocell	MAB EA 1 --
MAB A7-zinostatin conjugate	MAB EC708 -- Biovation
MAB ABX-RB2 -- Abgenix	MAB EP-5C7 -- Protein Design Labs
MAB ACA 11	MAB ERIC-1 -- ICRT
MAB AFP-I-131 -- Immunomedics	MAB F105 gene therapy
MAB AP1	MAB FC 2.15
MAB AZ1	MAB G250 -- Centocor
MAB B3-LysPE40 conjugate	MAB GA6
MAB B4 -- United Biomedical	MAB GA733
MAB B43 Genistein-conjugate	MAB Gliomab-H -- Viventia Biotech
MAB B43.13-Tc-99m -- Biomira	MAB HB2-saporin conjugate
MAB B43-PAP conjugate	MAB HD 37 --
MAB B4G7-gelonin conjugate	MAB HD37-ricin chain-A conjugate
MAB BCM 43-daunorubicin conjugate --	MAB HNK20 -- Acambis
BCM Oncologia	MAB huN901-DM1 conjugate --
MAB BIS-1	ImmunoGen
MAB BMS 181170 -- Bristol-Myers Squibb	MAB I-131 CC49 -- Corixa
MAB BR55-2	MAB ICO25
MAB BW494	MAB ICR12-CPG2 conjugate
MAB C 242-DM1 conjugate -- ImmunoGen	MAB ICR-62

## FIG. 1S

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MAb IRac-ricin A conjugate	MAb R-24
MAb K1	MAb R-24 $\alpha$ Human GD3 -- Celltech
MAb KS1-4-methotrexate conjugate	MAb RFB4-ricin chain A conjugate
MAb L6 -- Bristol-Myers Squibb, Oncogen	MAb RFT5-ricin chain A conjugate
MAb LICO 16-88	MAb SC 1
MAb LL2-I-131 -- Immunomedics	MAb SM-3 -- ICRT
MAb LL2-Y-90	MAb SMART 1D10 -- Protein Design Labs
MAb LS2D617 -- Hybritech	MAb SMART ABL 364 -- Novartis
MAb LYM-1-gelonin conjugate	MAb SN6f
MAb LYM-1-I-131	MAb SN6f-deglycosylated ricin A chain
MAb LYM-1-Y-90	conjugate --
MAb LYM-2 -- Peregrine	MAb SN6j
MAb M195	MAb SN7-ricin chain A conjugate
MAb M195-bismuth 213 conjugate --	MAb T101-Y-90 conjugate -- Hybritech
Protein Design Labs	MAb T-88 -- Chiron
MAb M195-gelonin conjugate	MAb TB94 -- Cancer ImmunoBiology
MAb M195-I-131	MAb TEC 11
MAb M195-Y-90	MAb TES-23 -- Chugai
MAb MA 33H1 -- Sanofi	MAb TM31 -- Avant
MAb MAD11	MAb TNT-1 -- Cambridge Antibody Tech.,
MAb Mgb2	Peregrine
MAb MINT5	MAb TNT-3
MAb MK2-23	MAb TNT-3 -- IL2 fusion protein --
MAb MOC31 ETA(252-613) conjugate	MAb TP3-At-211
MAb MOC-31-In-111	MAb TP3-PAP conjugate --
MAb MOC-31-PE conjugate	MAb UJ13A -- ICRT
MAb MR6 --	MAb UN3
MAb MRK-16 -- Aventis Pasteur	MAb ZME-018-gelonin conjugate
MAb MS11G6	MAB-BC2 -- GlaxoSmithKline
MAb MX-DTPA BrE-3	MAB-DM1 conjugate -- ImmunoGen
MAb MY9	MAB-ricin-chain-A conjugate -- XOMA
MAb Nd2 -- Tosoh	MAB-temoporphin conjugates
MAB NG-1 -- Hygeia	Monopharm C -- Viventia Biotech
MAB NM01 -- Nissin Food	monteplase -- Eisai
MAB OC 125	montirelin hydrate -- Gruenenthal
MAB OC 125-CMA conjugate	morotocog alfa -- Genetics Institute
MAB OKI-1 -- Ortho-McNeil	Morotocog-alfa -- Pharmacia
MAB OX52 -- Bioproducts for Science	MP 4
MAB PMA5	MP-121 -- Biopharm
MAB PR1	MP-52 -- Biopharm
MAB prost 30	MRA -- Chugai

FIG. 1T



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MS 28168 -- Mitsui Chemicals, Nihon Schering  
 MSH fusion toxin -- Ligand  
 MSI-99 -- Genaera  
 MT 201 -- Micromet  
 Muc-1 vaccine -- Corixa  
 mucosal tolerance -- Aberdeen  
 mullerian inhibiting subst  
 muplestim -- Genetics Institute, Novartis, DSM Anti-Infectives  
 murine MAB -- KS Biomedix  
 Mutant somatropin -- JCR Pharmaceutical  
 MV 833 -- Toagosei  
 Mycoplasma pulmonis vaccine  
 Mycoprex -- XOMA  
 myeloperoxidase -- Henogen  
 myostatin -- Genetics Institute  
 Naccolomab tafenatox -- Pharmacia  
 nagrestipen -- British Biotech  
 NAP-5 -- Corvas Intl.  
 NAPc2 -- Corvas Intl.  
 nartograstim -- Kyowa  
 Natalizumab -- Protein Design Labs  
 Nateplase -- NIH, Nihon Schering  
 nateplase -- Schering AG  
 NBI-3001 -- Neurocrine Biosci.  
 NBI-5788 -- Neurocrine Biosci.  
 NBI-6024 -- Neurocrine Biosci.  
 Nef inhibitors -- BRI  
 Neisseria gonorrhoea vaccine -- Antex Biologics  
 Neomycin B-arginine conjugate  
 Nerelimumab -- Chiron  
 Nerve growth factor -- Amgen -- Chiron, Genentech  
 Nerve growth factor gene therapy  
 nesiritide citrate -- Scios  
 neuregulin-2 -- CeNeS  
 neurocan -- NYU  
 neuronal delivery system -- CAMR  
 Neuroprotective vaccine -- University of Auckland  
 neurotrophic chimaeras -- Regeneron  
 neurotrophic factor -- NsGene, CereMedix  
 NeuroVax -- Immune Response  
 neuriturin -- Genentech  
 neutral endopeptidase -- Genentech  
 NGF enhancers -- NeuroSearch  
 NHL vaccine -- Large Scale Biology  
 NIP45 -- Boston Life Sciences  
 NKI-B20  
 NM 01 -- Nissin Food  
 NMI-139 -- NitroMed  
 NMMP -- Genetics Institute  
 NN-2211 -- Novo Nordisk  
 Noggin -- Regeneron  
 Nonacog alfa  
 Norelin -- Biostar  
 Norwalk virus vaccine  
 NRLU 10 -- NeoRx  
 NRLU 10 PE -- NeoRx  
 NT-3 -- Regeneron  
 NT-4/5 -- Genentech  
 NU 3056  
 NU 3076  
 NX 1838 -- Gilead Sciences  
 NY ESO-1/CAG-3 antigen -- NIH  
 NYVAC-7 -- Aventis Pasteur  
 NZ-1002 -- Novazyme  
 obesity therapy -- Nobex  
 OC 10426 -- Ontogen  
 OC 144093 -- Ontogen  
 OCIF -- Sankyo  
 Oct-43 -- Otsuka  
 OK PSA - liposomal  
 OKT3-gamma-1-ala-ala  
 OM 991  
 OM 992  
 Omalizumab -- Genentech  
 oncoimmunin-L -- NIH  
 Oncolysin B -- ImmunoGen

FIG. 1U

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Oncolysin CD6 -- ImmunoGen  
 Oncolysin M -- ImmunoGen  
 Oncolysin S -- ImmunoGen  
 Oncophage -- Antigenics  
 Oncostatin M -- Bristol-Myers Squibb  
 OncoVax-CL -- Jenner Biotherapies  
 OncoVax-P -- Jenner Biotherapies  
 oncept -- Yeda  
 onychomycosis vaccine -- Boehringer  
 Ingelheim  
 opebecan -- XOMA  
 opioids -- Arizona  
 Oprelvekin -- Genetics Institute  
 Org-33408 b-- Akzo Nobel  
 Orolip DP -- EpiCept  
 oryzacystatin  
 OSA peptides -- GenSci Regeneration  
 osteoblast-cadherin GF -- Pharis  
 Osteocalcin-thymidine kinase gene therapy  
 osteogenic protein -- Curis  
 osteopontin -- OraPharma  
 osteoporosis peptides -- Integra, Telios  
 osteoprotegerin -- Amgen, SnowBrand  
 otitis media vaccines -- Antex Biologics  
 ovarian cancer -- University of Alabama  
 OX40-IgG fusion protein -- Cantab, Xenova  
 P 246 -- Diatide  
 P 30 -- Alfacell  
 p1025 -- Active Biotech  
 P-113<sup>A</sup> -- Demegen  
 P-16 peptide -- Transition Therapeutics  
 p43 -- Ramot  
 P-50 peptide -- Transition Therapeutics  
 p53 + RAS vaccine -- NIH, NCI  
 PACAP(1-27) analogue  
 paediatric vaccines -- Chiron  
 Pafase -- ICOS  
 PAGE-4 plasmid DNA -- IDEC  
 PAI-2 -- Biotech Australia, Human  
 Therapeutics  
 Palivizumab -- MedImmune  
 PAM 4 -- Merck  
 pamiteplase -- Yamanouchi  
 pancreatin, Minitabs -- Eurand  
 Pangen -- Fournier  
 Pantarin -- Selective Genetics  
 Parainfluenza virus vaccine -- Pharmacia,  
 Pierre Fabre  
 paraoxanase -- Esperion  
 parathyroid hormone -- Abiogen, Korea  
 Green Cross  
 Parathyroid hormone (1-34) --  
 Chugai/Suntory  
 Parkinson's disease gene therapy -- Cell  
 Genesys/ Ceregene  
 Parvovirus vaccine -- MedImmune  
 PCP-Scan -- Immunomedics  
 PDGF cocktail -- Theratechnologies  
 peanut allergy therapy -- Dynavax  
 PEG anti-ICAM MAb -- Boehringer  
 Ingelheim  
 PEG asparaginase -- Enzon  
 PEG glucocerebrosidase  
 PEG hirudin -- Knoll  
 PEG interferon-alpha-2a -- Roche  
 PEG interferon-alpha-2b + ribavirin --  
 Biogen, Enzon, ICN Pharmaceuticals,  
 Schering-Plough  
 PEG MAb A5B7 --  
 Pegacaristim -- Amgen -- Kirin Brewery --  
 ZymoGenetics  
 Pegaldesleukin -- Research Corp  
 pegaspargase -- Enzon  
 pegfilgrastim -- Amgen  
 PEG-interferon Alpha -- Viragen  
 PEG-interferon Alpha 2A -- Hoffman La-  
 Roche  
 PEG-interferon Alpha 2B -- Schering-  
 Plough  
 PEG-r-hirudin -- Abbott  
 PEG-uricase -- Mountain View  
 Pegvisomant -- Genentech

FIG. 1V

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PEGylated proteins, PolyMASC -- Valentis Pharmaprojects No. 5947 -- StressGen  
 PEGylated recombinant native human leptin Pharmaprojects No. 5961 --  
 -- Roche Theratechnologies  
 Pentumomab Pharmaprojects No. 5962 -- NIH  
 Penetratin -- Cyclacel Pharmaprojects No. 5966 -- NIH  
 Pepsican -- Antisoma Pharmaprojects No. 5994 -- Pharming  
 peptide G -- Peptech, ICRT Pharmaprojects No. 5995 -- Pharming  
 peptide vaccine -- NIH, NCRI Pharmaprojects No. 6023 -- IMMUCON  
 Pexelizumab Pharmaprojects No. 6063 -- Cytoclonal  
 pexiganan acetate -- Genatera Pharmaprojects No. 6073 -- SIDDCO  
 Pharmaprojects No. 3179 -- NYU Pharmaprojects No. 6115 -- Genzyme  
 Pharmaprojects No. 3390 -- Ernest Orlando Pharmaprojects No. 6227 -- NIH  
 Pharmaprojects No. 3417 -- Sumitomo Pharmaprojects No. 6230 -- NIH  
 Pharmaprojects No. 3777 -- Acambis Pharmaprojects No. 6236 -- NIH  
 Pharmaprojects No. 4209 -- XOMA Pharmaprojects No. 6243 -- NIH  
 Pharmaprojects No. 4349 -- Baxter Intl. Pharmaprojects No. 6244 -- NIH  
 Pharmaprojects No. 4651 Pharmaprojects No. 6281 -- Senetek  
 Pharmaprojects No. 4915 -- Avanir Pharmaprojects No. 6365 -- NIH  
 Pharmaprojects No. 5156 -- Rhizogenics Pharmaprojects No. 6368 -- NIH  
 Pharmaprojects No. 5200 -- Pfizer Pharmaprojects No. 6373 -- NIH  
 Pharmaprojects No. 5215 -- Origene Pharmaprojects No. 6408 -- Pan Pacific  
 Pharmaprojects No. 5216 -- Origene Pharmaprojects No. 6410 -- Athensys  
 Pharmaprojects No. 5218 -- Origene Pharmaprojects No. 6421 -- Oxford  
 Pharmaprojects No. 5267 -- ML GlycoSciences  
 Laboratories Pharmaprojects No. 6522 -- Maxygen  
 Pharmaprojects No. 5373 -- MorphoSys Pharmaprojects No. 6523 -- Pharis  
 Pharmaprojects No. 5493 -- Metabolex Pharmaprojects No. 6538 -- Maxygen  
 Pharmaprojects No. 5707 -- Genentech Pharmaprojects No. 6554 -- APALEXO  
 Pharmaprojects No. 5728 -- Autogen Pharmaprojects No. 6560 -- Ardana  
 Pharmaprojects No. 5733 -- BioMarin Pharmaprojects No. 6562 -- Bayer  
 Pharmaprojects No. 5757 -- NIH Pharmaprojects No. 6569 -- Eos  
 Pharmaprojects No. 5765 -- Gryphon Phenoxazine  
 Pharmaprojects No. 5830 -- AntiCancer Phenylase -- Ibex  
 Pharmaprojects No. 5839 -- Dyax Pigment epithelium derived factor --  
 Pharmaprojects No. 5849 -- Johnson & plasminogen activator inhibitor-1,  
 Johnson recombinant -- DuPont Pharmaceuticals  
 Pharmaprojects No. 5860 -- Mitsubishi-  
 Tokyo  
 Pharmaprojects No. 5869 -- Oxford  
 GlycoSciences  
 Pharmaprojects No. 5883 -- Asahi Brewery

FIG. 1W

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Plasminogen activators -- Abbott  
 Laboratories, American Home Products,  
 Boehringer Mannheim, Chiron  
 Corporation, DuPont Pharmaceuticals, Eli  
 Lilly, Shionogi, Genentech, Genetics  
 Institute, GlaxoSmithKline, Hemispherx  
 Biopharma, Merck & Co, Novartis,  
 Pharmacia Corporation, Wakamoto, Yeda  
 plasminogen-related peptides -- Bio-Tech.  
 General/MGH  
 platelet factor 4 -- RepliGen  
 Platelet-derived growth factor -- Amgen --  
 ZymoGenetics  
 plusonmerin-- Hayashibara  
 PMD-2850 -- Protherics  
 Pneumococcal vaccine -- Antex Biologics,  
 Aventis Pasteur  
 Pneumococcal vaccine intranasal --  
 BioChem Vaccines/Biovector  
 PR1A3  
 PR-39  
 pralmorelin -- Kaken  
 Pretarget-Lymphoma -- NeoRx  
 Priliximab -- Centocor  
 PRO 140 -- Progenics  
 PRO 2000 -- Procept  
 PRO 367 -- Progenics  
 PRO 542 -- Progenics  
 pro-Apo A-I -- Esperion  
 prolactin -- Genzyme  
 Prosaptide TX14(A) -- Bio-Tech. General  
 prostate cancer antibodies -- Immunex,  
 UroCor  
 prostate cancer antibody therapy --  
 Genentech/UroGenesys,  
 Genotherapeutics  
 prostate cancer immunotherapeutics -- The  
 PSMA Development Company  
 prostate cancer vaccine -- Aventis Pasteur,  
 Zonagen, Corixa, Dendreon, Jenner  
 Biotherapies, Therion Biologics  
 prostate-specific antigen -- Entremed  
 protein A -- RepliGen  
 protein adhesives -- Enzon  
 protein C -- Baxter Intl., PPL Therapeutics,  
 ZymoGenetics  
 protein C activator -- Gilead Sciences  
 protein kinase R antagonists -- NIH  
 protirelin -- Takeda  
 protocadherin 2 -- Caprion  
 Pro-urokinase -- Abbott, Bristol-Myers  
 Squibb, Dainippon, Tosoh -- Welfide  
 P-selectin glycoprotein ligand-1 -- Genetics  
 Institute  
 pseudomonal infections -- InterMune  
 Pseudomonas vaccine -- Cytovax  
 PSGL-Ig -- American Home Products  
 PSP-94 -- Procyon  
 PTH 1-34 -- Nobex  
 Quilimmune-M -- Antigenics  
 R 101933  
 R 125224 -- Sankyo  
 RA therapy -- Cardion  
 Rabies vaccine recombinant -- Aventis  
 Pasteur, BioChem Vaccines, Kaketsuken  
 Pharmaceuticals  
 RadioTheraCIM -- YM BioSciences  
 Ramot project No. 1315 -- Ramot  
 Ramot project No. K-734A -- Ramot  
 Ramot project No. K-734B -- Ramot  
 RANK -- Immunex  
 ranpimase -- Alfacell  
 ranpimase-anti-CD22 Mab -- Alfacell  
 RANTES inhibitor -- Milan  
 RAPID drug delivery systems -- ARIAD  
 rasburicase -- Sanofi  
 rBPI-21, topical -- XOMA  
 RC 529 -- Corixa  
 rCFTR -- Genzyme Transgenics  
 RD 62198  
 rDnase -- Genentech  
 RDP-58 -- SangStat

FIG. 1X

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RecepTox-Fce -- Keryx	Ribozyme gene therapy -- Genset
RecepTox-GnRH -- Keryx, MTR Technologies	Rickettsial vaccine recombinant
RecepTox-MBP -- Keryx, MTR Technologies	RIGScan CR -- Neoprobe
recFSH -- Akzo Nobel, Organon	RIP-3 -- Rigel
REGA 3G12	RK-0202 -- RxKinetix
Regavirumab -- Teijin	RLT peptide -- Esperion
relaxin -- Connetics, Corp	rMNEI -- IVAX
Renal cancer vaccine -- Macropharm	rmCRP -- Immtech
repifermin -- Human Genome Sciences	RN-1001 -- Renovo
Respiratory syncytial virus PFP-2 vaccine -- Wyeth-Lederle	RN-3 -- Renovo
Respiratory syncytial virus vaccine -- GlaxoSmithKline, Pharmacia, Pierre Fabre	RNAse conjugate -- Immunomedics
Respiratory syncytial virus vaccine inactivated	RO 631908 -- Roche
Respiratory syncytial virus-parainfluenza virus vaccine -- Aventis Pasteur, Pharmacia	Rotavirus vaccine -- Merck
Reteplase -- Boehringer Mannheim, Hoffman La-Roche	RP 431 -- DuPont Pharmaceuticals
Retropep -- Retroscreen	RP-128 -- Resolution
RFB4 (dsFv) PE38	RPE65 gene therapy --
RFI 641 -- American Home Products	RPR 110173 -- Aventis Pasteur
RFTS -- UAB Research Foundation	RPR 115135 -- Aventis Pasteur
RG 12986 -- Aventis Pasteur	RPR 116258A -- Aventis Pasteur
RG 83852 -- Aventis Pasteur	rPSGL-Ig -- American Home Products
RG-1059 -- RepliGen	r-SPC surfactant -- Byk Gulden
rGCR -- NIH	rV-HER-2/neu -- Theron Biologics
rGLP-1 -- Restoragen	SA 1042 -- Sankyo
rGRF -- Restoragen	sacrosidase -- Orphan Medical
rh Insulin -- Eli Lilly	Sant 7
RHAMM targeting peptides -- Cangene	Sargramostim -- Immunex
rHb1.1 -- Baxter Intl.	saruplase -- Gruenenthal
rhCC10 -- Claragen	Satumomab -- Cytogen
rhCG -- Sero	SB 1 -- COR Therapeutics
Rheumatoid arthritis gene therapy	SB 207448 -- GlaxoSmithKline
Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB 208651 -- GlaxoSmithKline
rhLH -- Sero	SB 240683 -- GlaxoSmithKline
	SB 249415 -- GlaxoSmithKline
	SB 249417 -- GlaxoSmithKline
	SB 6 -- COR Therapeutics
	SB RA 31012 --
	SC 56929 -- Pharmacia
	SCA binding proteins -- Curis, Enzon
	scFv(14E1)-ETA Berlex Laboratories,
	Schering AG
	ScFv(FRP5)-ETA --

FIG. 1Y

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ScFv6C6-PE40 --  
 SCH 55700 -- Celltech  
 Schistosomiasis vaccine -- Glaxo  
 Wellcome/Medeve, Brazil  
 SCPF -- Advanced Tissue Sciences  
 scuPA-suPAR complex -- Hadasit  
 SD-9427 -- Pharmacia  
 SDF-1 -- Ono  
 SDZ 215918 -- Novartis  
 SDZ 280125 -- Novartis  
 SDZ 89104 -- Novartis  
 SDZ ABL 364 -- Novartis  
 SDZ MMA 383 -- Novartis  
 serine protease inhibs -- Pharis  
 sermorelin acetate -- Serono  
 SERP-1 -- Viron  
 serteneff -- Dainippon  
 serum albumin, Recombinant human --  
 Aventis Behring  
 serum-derived factor -- Hadasit  
 Sevrumab -- Novartis  
 SGN 14 -- Seattle Genetics  
 SGN 15 -- Seattle Genetics  
 SGN 17/19 -- Seattle Genetics  
 SGN 30 -- Seattle Genetics  
 SGN-10 -- Seattle Genetics  
 SGN-11 -- Seattle Genetics  
 SH 306 -- DuPont Pharmaceuticals  
 Shanvac-B -- Shantha  
 Shigella flexneri vaccine -- Avant, Acambis,  
 Novavax  
 Shigella sonnei vaccine --  
 siCAM-1 -- Boehringer Ingelheim  
 Silteplase -- Genzyme  
 SIV vaccine -- Endocon, Institut Pasteur  
 SK 896 -- Sanwa Kagaku Kenkyusho  
 SK-827 -- Sanwa Kagaku Kenkyusho  
 Skeletex -- CellFactors  
 SKF 106160 -- GlaxoSmithKline  
 S-nitroso-AR545C --  
 SNTP -- Active Biotech  
 somatomedin-1 -- GroPep, Mitsubishi-  
 Tokyo, NIH  
 somatomedin-1 carrier protein -- Insmed  
 somatostatin -- Ferring  
 Somatotropin/  
 Human Growth Hormone -- Bio-Tech.  
 General, Eli Lilly  
 somatropin -- Bio-Tech. General, Alkermes,  
 ProLease, Aventis Behring, Biovector,  
 Cangene, Dong-A, Eli Lilly, Emisphere,  
 Enact, Genentech, Genzyme Transgenics,  
 Grandis/InfiMed, CSL, InfiMed, MacroMed,  
 Novartis, Novo Nordisk, Pharmacia  
 Serono, TranXenoGen  
 somatropin derivative -- Schering AG  
 somatropin, AIR -- Eli Lilly  
 Somatropin, inhaled -- Eli Lilly/Alkermes  
 somatropin, Kabi -- Pharmacia  
 somatropin, Orasome -- Novo Nordisk  
 Sonermin -- Dainippon Pharmaceutical  
 SP(V5.2)C -- Supertek  
 SPf66  
 sphingomyelinase -- Genzyme  
 SR 29001 -- Sanofi  
 SR 41476 -- Sanofi  
 SR-29001 -- Sanofi  
 SS1(dsFV)-PE38 -- NeoPharm  
 $\beta$ 2 microglobulin -- Avidex  
 $\beta$ 2-microglobulin fusion proteins -- NIH  
 $\beta$ -amyloid peptides -- CeNeS  
 $\beta$ -defensin -- Pharis  
 Staphylococcus aureus infections --  
 InhibiteX/ZLB  
 Staphylococcus aureus vaccine conjugate --  
 Nabi  
 Staphylococcus therapy -- Tripep  
 Staphylokinase -- Biovation, Prothera,  
 Thrombogenetics  
 Streptococcal A vaccine -- M6  
 Pharmaceuticals, North American Vaccine  
 Streptococcal B vaccine -- Microscience

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Streptococcal B vaccine recombinant --  
 Biochem Vaccines  
 Streptococcus pyogenes vaccine  
 STRL-33 -- NIH  
 Subalin -- SRC VB VECTOR  
 SUI5 -- United Biomedical  
 SUI5-LHRH -- United Biomedical  
 SUN-E3001 -- Suntory  
 super high affinity monoclonal antibodies --  
 YM BioSciences  
 Superoxide dismutase -- Chiron, Enzon,  
 Ube Industries, Bio-Tech, Yeda  
 superoxide dismutase-2 -- OXIS  
 suppressin -- UAB Research Foundation  
 SY-161-P5 -- ThromboGenics  
 SY-162 -- ThromboGenics  
 Systemic lupus erythematosus vaccine --  
 MedClone/VivoRx  
 T cell receptor peptide vaccine  
 T4N5 liposomes -- AGI Dermatics  
 TACI, soluble -- ZymoGenetics  
 targeted apoptosis -- Antisoma  
 tasonermin -- Boehringer Ingelheim  
 TASP  
 TASP-V  
 Tat peptide analogues -- NIH  
 TBP I -- Yeda  
 TBP II  
 TBV25H -- NIH  
 Tc 99m lor cea1 -- Center of Molecular  
 Immunology  
 Tc 99m P 748 -- Diatide  
 Tc 99m votumumab -- Intracell  
 Tc-99m rh-Annexin V -- Theseus Imaging  
 teceleukin -- Biogen  
 tenecteplase -- Genentech  
 Teriparatide -- Armour Pharmaceuticals,  
 Asahi Kasei, Eli Lilly  
 terlipressin -- Ferring  
 testisin -- AMRAD  
 Tetrafibricin -- Roche  
 TFPI -- EntreMed  
 tgD-IL-2 -- Takeda  
 TGF-Alpha -- ZymoGenetics  
 TGF- $\beta$  -- Kolon  
 TGF- $\beta$ 2 -- Insmed  
 TGF- $\beta$ 3 -- OSI  
 Thalassaemia gene therapy -- Crucell  
 TheraCIM-h-R3 -- Center of Molecular  
 Immunology, YM BioSciences  
 Theradigm-HBV -- Epimmune  
 Theradigm-HPV -- Epimmune  
 Theradigm-malaria -- Epimmune  
 Theradigm-melanoma -- Epimmune  
 TheraFab -- Antisoma  
 ThGRF 1-29 -- Theratechnologies  
 ThGRF 1-44 -- Theratechnologies  
 thrombomodulin -- Iowa, Novocastra  
 Thrombopoietin -- Dragon Pharmaceuticals,  
 Genentech  
 thrombopoietin, Pliva -- Recepton  
 Thrombospondin 2 --  
 thrombostatin -- Thromgen  
 thymalfasin -- SciClone  
 thymocartin -- Gedeon Richter  
 thymosin Alpha1 -- NIH  
 thyroid stimulating hormone -- Genzyme  
 tICAM-1 -- Bayer  
 Tick anticoagulant peptide -- Merck  
 TIF -- Xoma  
 Tifacogin -- Chiron, NIS, Pharmacia  
 Tissue factor -- Genentech  
 Tissue factor pathway inhibitor  
 TJN-135 -- Tsumura  
 TM 27 -- Avant  
 TM 29 -- Avant  
 TMC-151 -- Tanabe Seiyaku  
 TNF tumour necrosis factor -- Asahi Kasei  
 TNF Alpha -- Cytimmune  
 TNF antibody -- Johnson & Johnson  
 TNF binding protein -- Amgen  
 TNF degradation product -- Oncotech

FIG. 1AA

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TNF receptor -- Immunex	TXU-PAP
TNF receptor 1, soluble -- Amgen	TY-10721 -- TOA Eiyo
TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genentech, Mochida	Type I diabetes vaccine -- Research Corp
TNF-Alpha inhibitor -- Tripep	Typhoid vaccine CVD 908
TNFR:Fc gene therapy -- Targeted Genetics	U 143677 -- Pharmacia
TNF-SAM2	U 81749 -- Pharmacia
Tolerimab -- Innogenetics	UA 1248 -- Arizona
Toxoplasma gondii vaccine -- GlaxoSmithKline	UGIF -- Sheffield
TP 9201 -- Telios	UIC 2
TP10 -- Avant	UK 101
TP20 -- Avant	UK-279276 -- Corvas Intl.
tPA -- Centocor	urodilatin -- Pharis
trafermin -- Scios	urofolitrophin -- Serono
TRAIL/Apo2L -- Immunex	uteroferrin -- Pepgen
transferrin-binding proteins -- CAMR	V 20 -- GLYCODEsign
Transforming growth factor-beta-1 -- Genentech	V2 vasopressin receptor gene therapy vaccines -- Active Biotech
transport protein -- Genesis	Varicella zoster glycoprotein vaccine -- Research Corporation Technologies
TRH -- Ferring	Varicella zoster virus vaccine live -- Cantab Pharmaceuticals
Triabin -- Schering AG	Vascular endothelial growth factor -- Genentech, University of California
Triconal	Vascular endothelial growth factors -- R&D Systems
Triflavin	vascular targeting agents -- Peregrine
troponin I -- Boston Life Sciences	vasopermeation enhancement agents -- Peregrine
TRP-2 <sup>A</sup> -- NIH	vasostatin -- NIH
trypsin inhibitor -- Mochida	VCL -- Bio-Tech. General
TSP-1 gene therapy --	VEGF -- Genentech, Scios
TT-232	VEGF inhibitor -- Chugai
TTS-CD2 -- Active Biotech	VEGF-2 -- Human Genome Sciences
Tuberculosis vaccine -- Aventis Pasteur, Genesis	VEGF-Trap -- Regeneron
Tumor Targeted Superantigens -- Active Biotech -- Pharmacia	viscumin, recombinant -- Madaus
tumour vaccines -- PhotoCure	Vitaxin
tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen	Vitrax -- ISTA Pharmaceuticals
tumstatin -- ILEX	West Nile virus vaccine -- Bavarian Nordic
Tuvirumab -- Novartis	WP 652
TV-4710 -- Teva	WT1 vaccine -- Corixa
TWEAK receptor -- Immunex	WX-293 -- Willex BioTech.

FIG. 1BB



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WX-360 -- Wilex BioTech.	YM 207 -- Yamanouchi
WX-UK1 -- Wilex BioTech.	YM 337 -- Protein Design Labs
XMP-500 -- XOMA	Yttrium-90 labelled biotin
XomaZyme-791 -- XOMA	Yttrium-90-labeled anti-CEA MAb T84.66 --
XTL 001 -- XTL Biopharmaceuticals	ZD 0490 -- AstraZeneca
XTL 002 -- XTL Biopharmaceuticals	ziconotide -- Elan
yeast delivery system -- GlobelImmune	ZK 157138 -- Berlex Laboratories
Yersinia pestis vaccine	Zollmombab aritox
YIGSR-Stealth -- Johnson & Johnson	Zorcell -- Immune Response
Yisum Project No. D-0460 -- Yisum	ZRXL peptides -- Novartis

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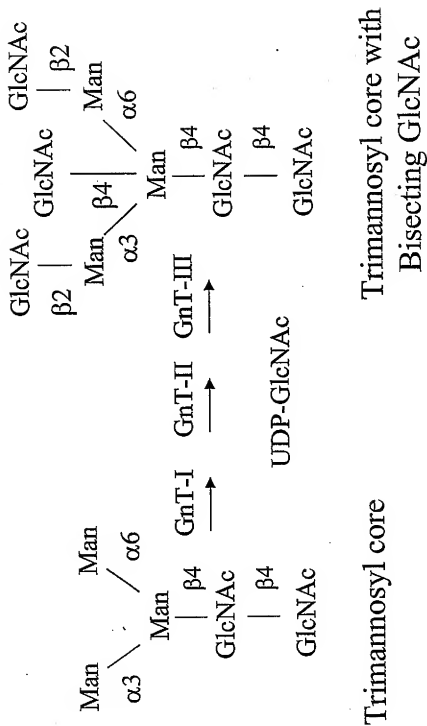
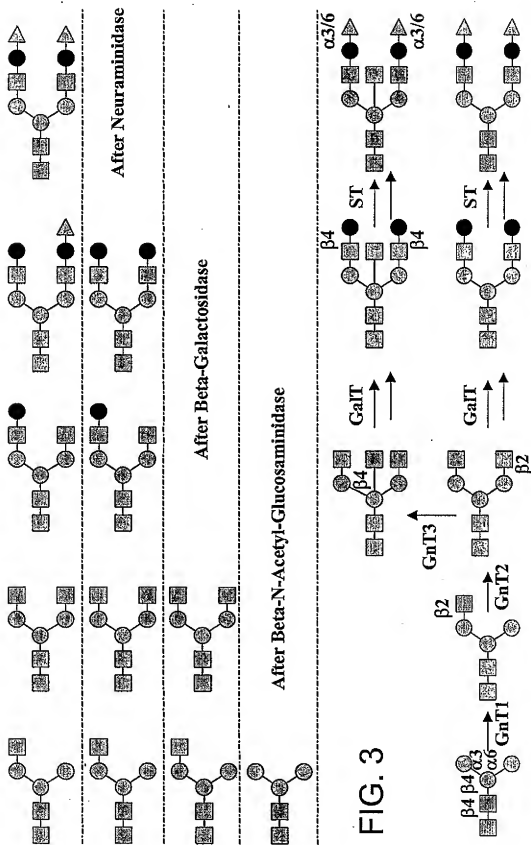


FIG. 2

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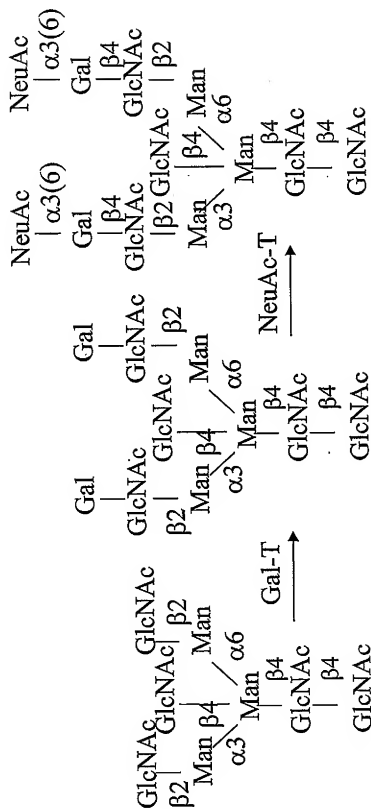


FIG. 4

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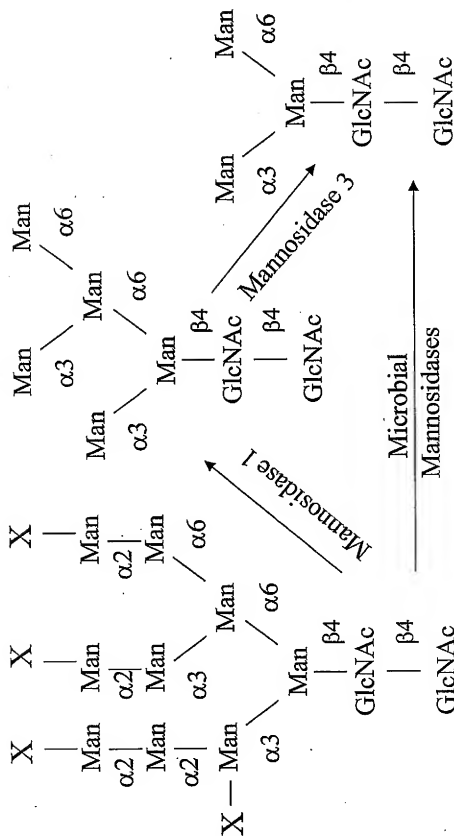


FIG. 5

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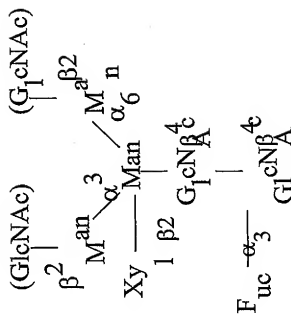


FIG. 6

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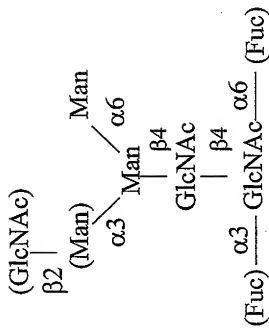


FIG. 7

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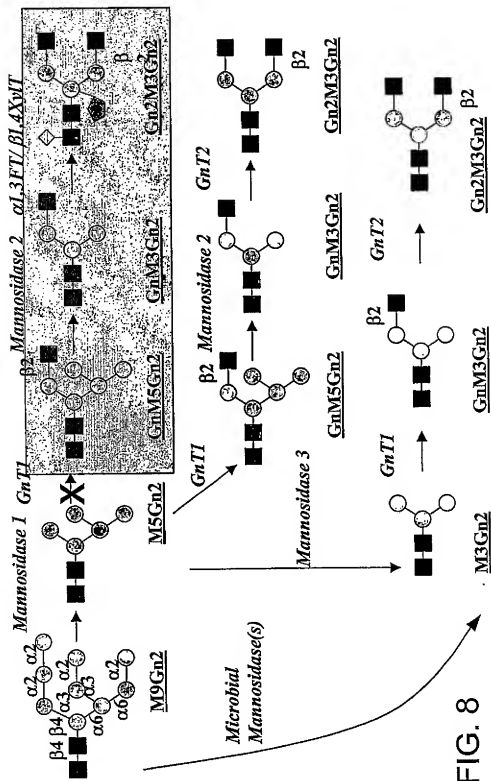


FIG. 8



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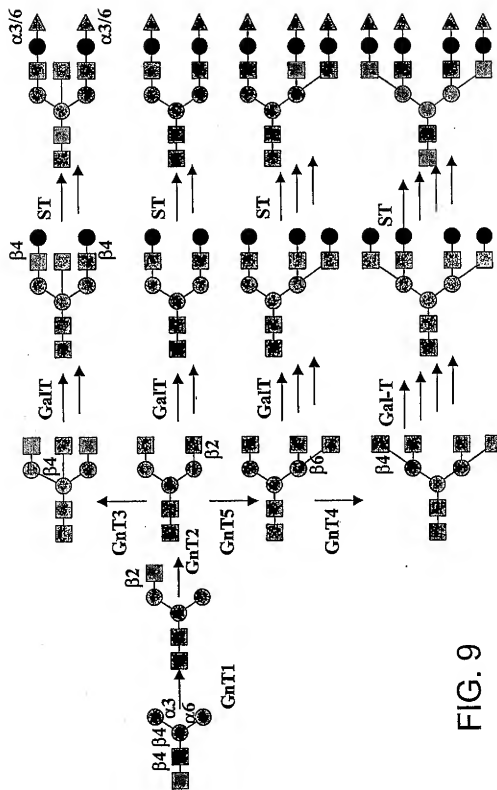


FIG. 9



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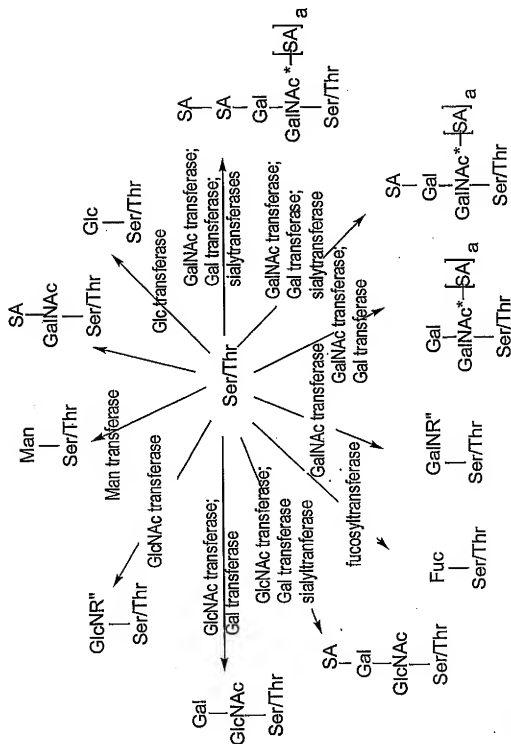


FIG. 11

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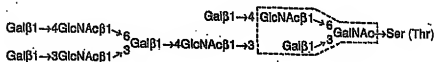
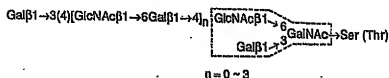
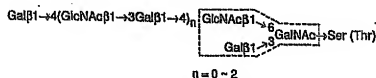
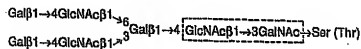
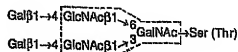
*Core 1**Core 2**Core 3**Core 4*

FIG. 12



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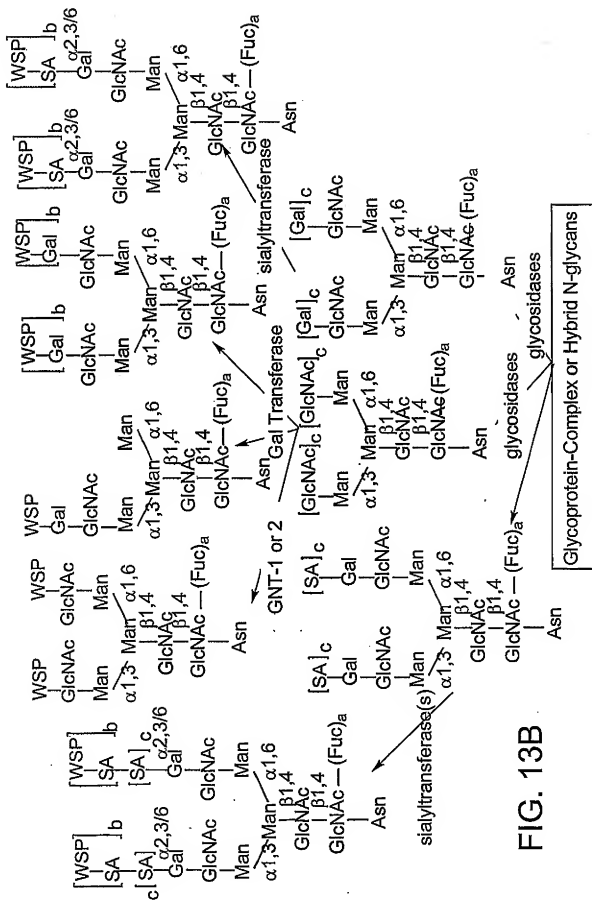


FIG. 13B

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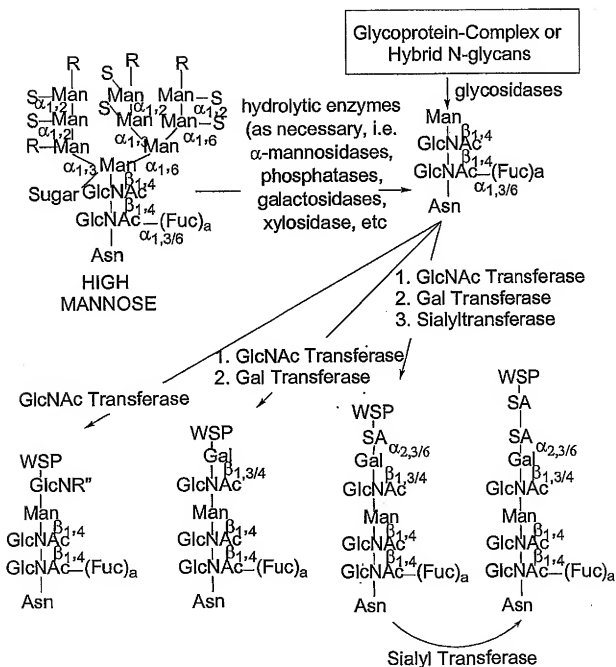


FIG. 14





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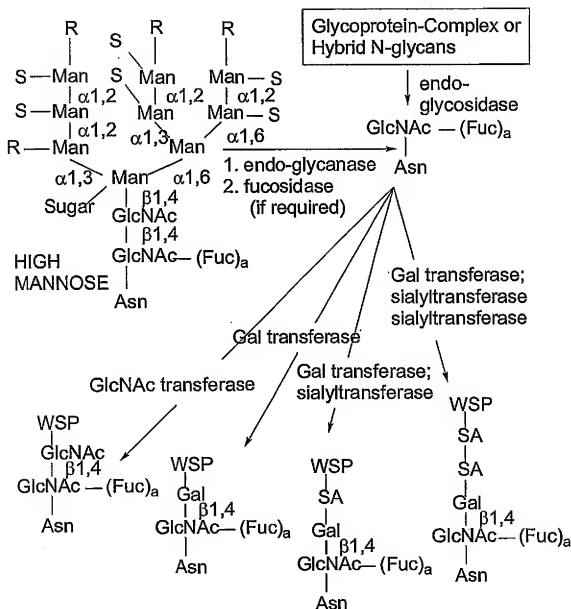


FIG. 16









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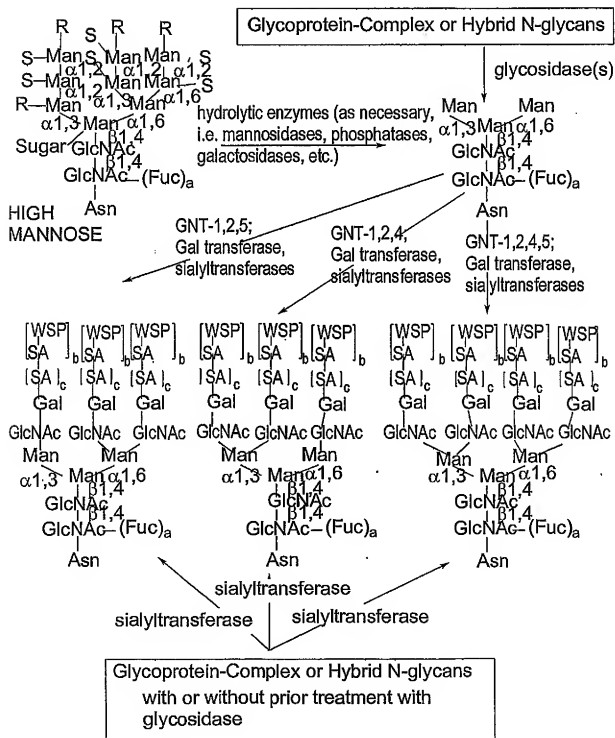


FIG. 19

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## O-LINKED OLIGOSACCHARIDES

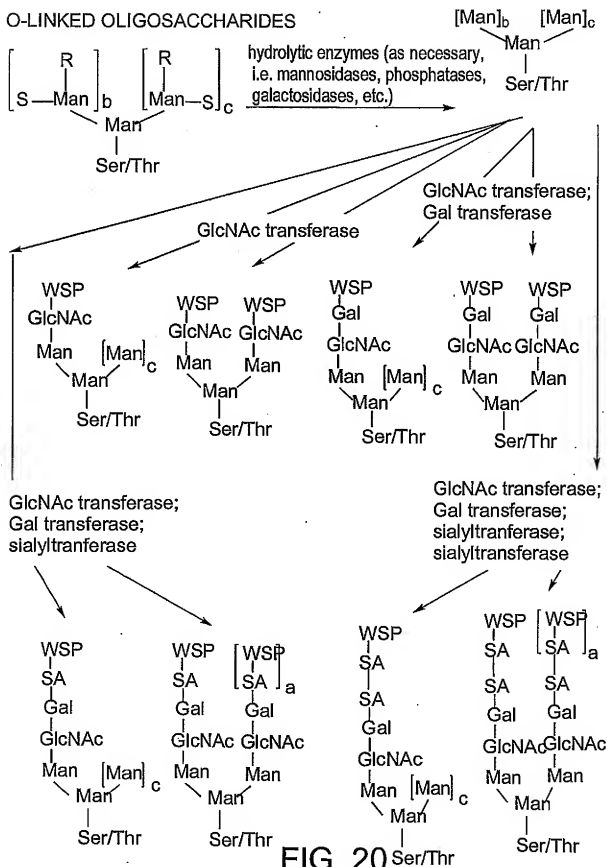


FIG. 20

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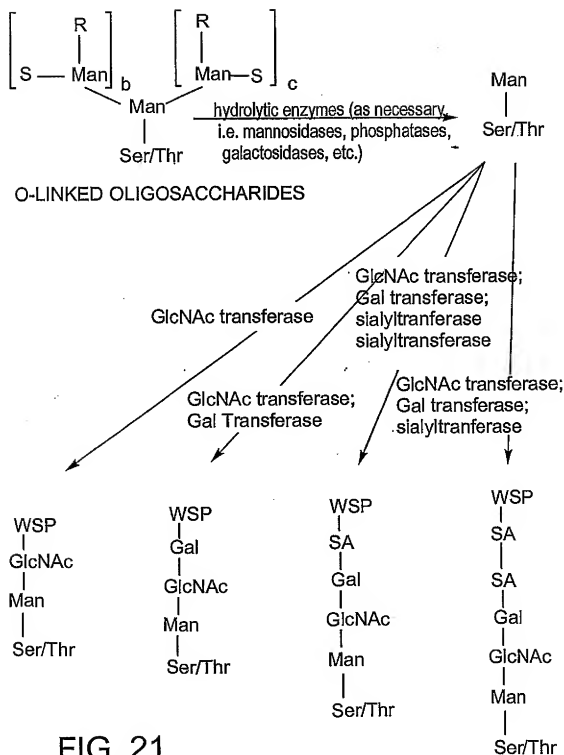


FIG. 21



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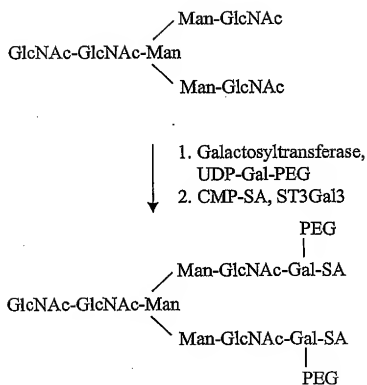


FIG. 22A

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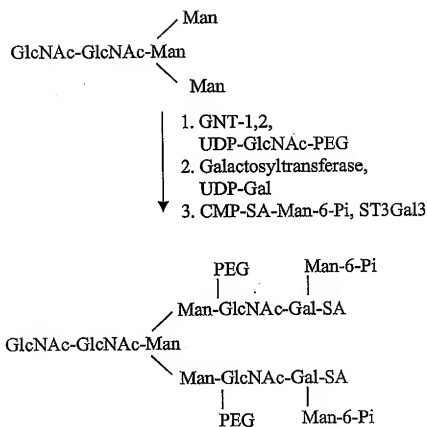


FIG. 22B

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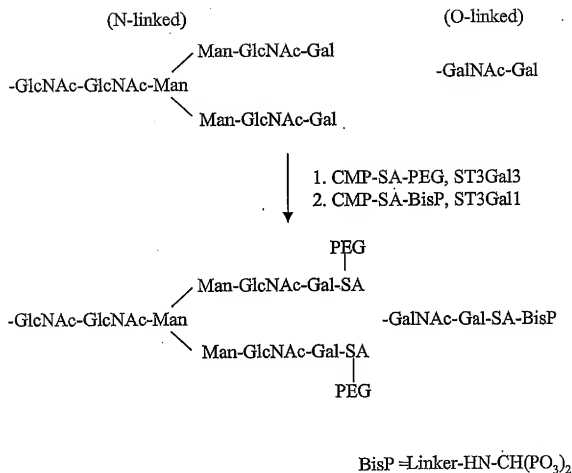


FIG. 22C

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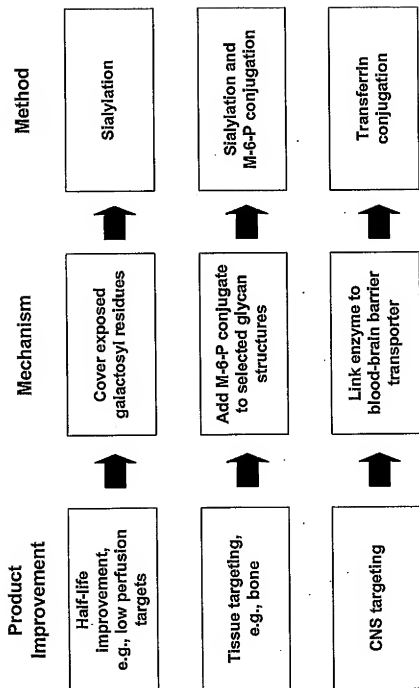


FIG. 23

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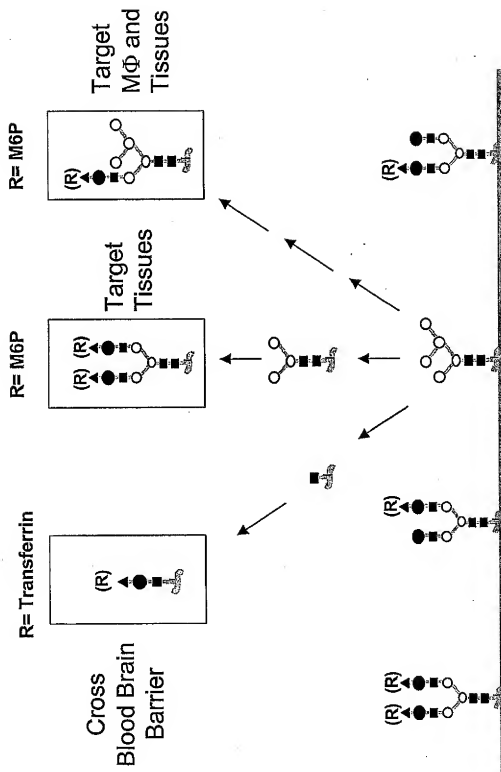


FIG. 24

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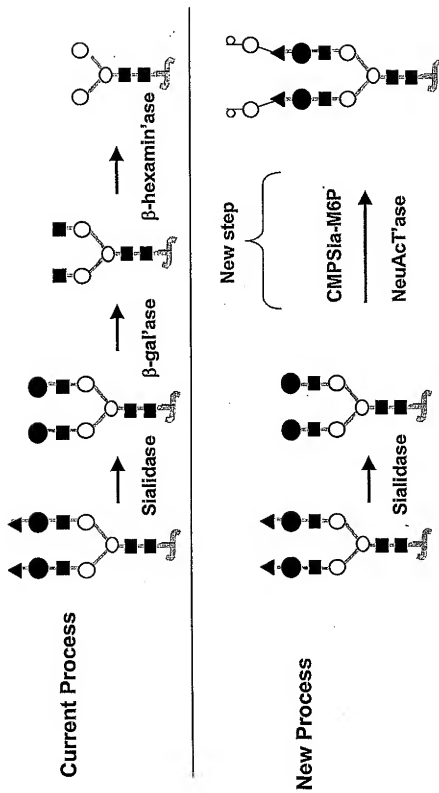


FIG. 25

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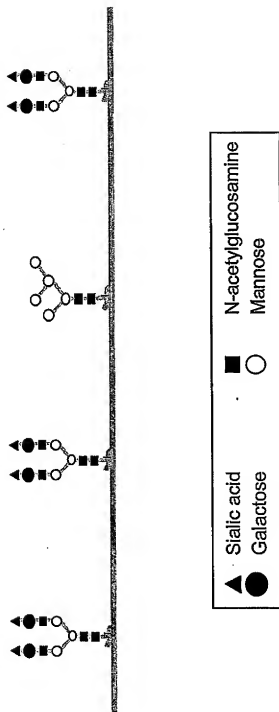
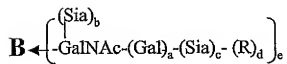
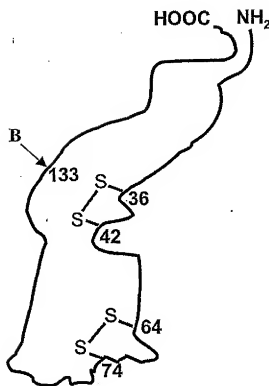


FIG. 26

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose

FIG. 27A



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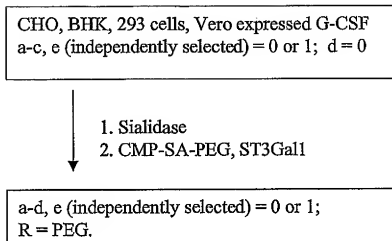


FIG. 27B

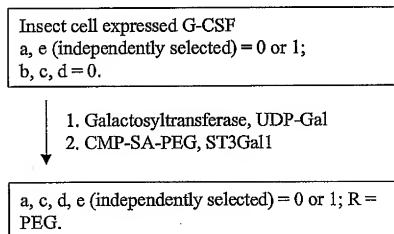


FIG. 27C

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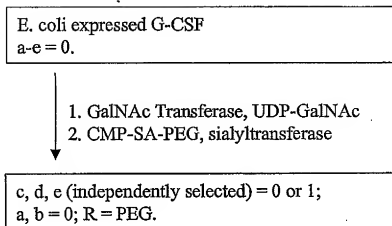


FIG. 27D

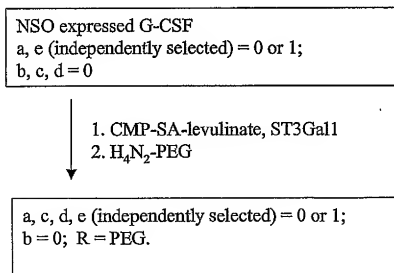


FIG. 27E

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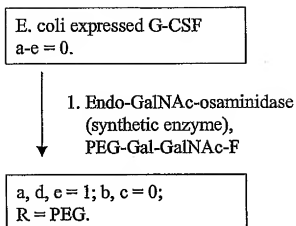


FIG. 27F

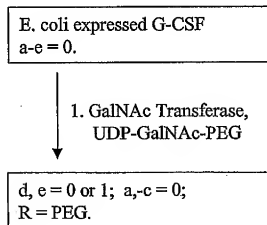
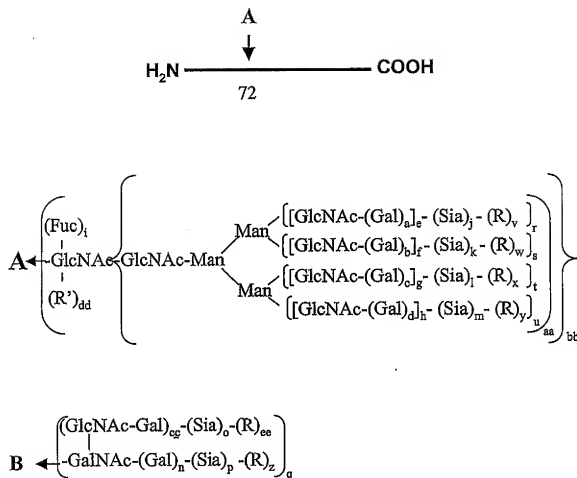


FIG. 27G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 28A

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CHO, BHK, 293 cells, Vero expressed  
interferon alpha 14C.  
a-d, aa, bb = 1; e-h = 1 to 4;  
cc, j-m, i, r-u (independently selected) = 0 or 1;  
q, n-p, v-z, cc, dd, ee = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

a-d, aa, bb = 1; e-h = 1 to 4;  
bb, cc, i, r-u (independently selected) = 0 or 1;  
q, n-p, v-z, cc, dd, ee = 0;  
v-y (independently selected) = 1,  
when j-m (independently selected) = 1;  
R = PEG.

FIG. 28B

Insect cell or fungi expressed interferon alpha-14C.  
a-d, f, h, j-q, s, u, v-z, cc, dd, ee = 0;  
e, g, i, r, t (independently selected) = 0 or 1;  
aa, bb = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal-PEG

b, d, f, h, j-q, s, u, w, y, z, cc, dd, ee = 0;  
a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;  
v, x (independently selected) = 1,  
when a, c, (independently selected) = 1;  
aa, bb = 1; R = PEG.

FIG. 28C

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Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

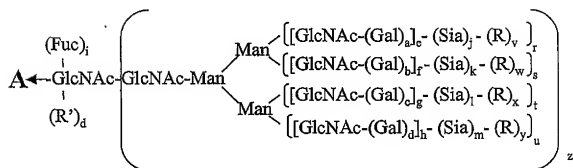
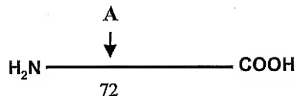
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 28D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 28E

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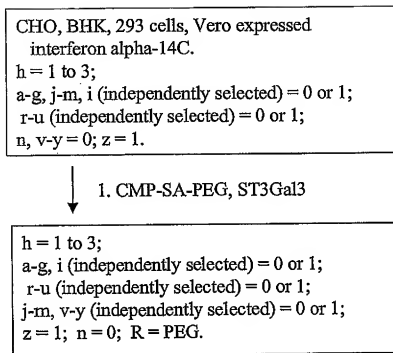


FIG. 28F

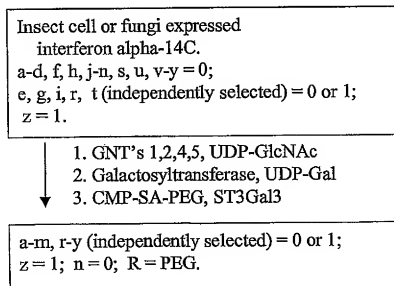


FIG. 28G



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Yeast expressed interferon alpha-14C.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1; R (branched or linear) = Man,  
oligomannose.

1. mannosidases

2. GNT's 1,2,4,5, UDP-GlcNAc

3. Galactosyltransferase, UDP-Gal

4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 28H

NSO expressed interferon alpha 14C.

a-i, r-u (independently selected) = 0 or 1;

j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt

2. H<sub>4</sub>N<sub>2</sub>-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;

n = 0; z = 1; R = PEG.

FIG. 28I

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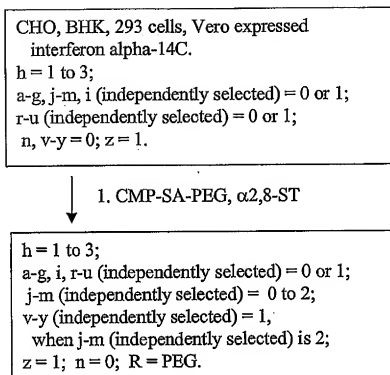


FIG. 28J

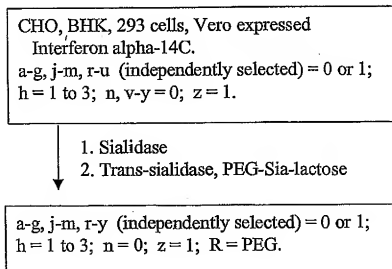


FIG. 28K

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CHO, BHK, 293 cells, Vero expressed  
interferon alpha-14C.

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

1. CMP-SA,  $\alpha$ 2,8-ST

h = 1 to 3;

a-g, i, r-u (independently selected) = 0 or 1;

j-m (independently selected) = 0 to 40;

z = 1; v-y, n = 0.

FIG. 28L

Insect cell or fungi expressed interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1;

z = 1.

1. GNT's 1 & 2, UDP-GlcNAc

2. Galactosyltransferase,

UDP-Gal-linker-SA-CMP

3. ST3Gal3, transferrin

a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;

z = 1; b, d, f, h, j-n, s, u, w, y = 0;

R = transferrin.

FIG. 28M

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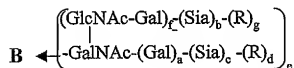
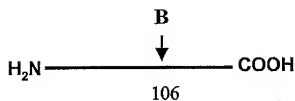
Insect cell or fungi expressed interferon alpha-14C.  
a-d, f, h, j-n, s, u, v-y = 0;  
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
  2. Galactosyltransferase,  
UDP-Gal-linker-SA-CMP
  3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;  
a-h, j-m, r-z = 0;  
n = 1; R' = -Gal-linker-transferrin.

FIG. 28N

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a-c, e, f (independently selected) = 0 or 1;  
 d, g = 0; R = polymer, glycoconjugate.

FIG. 280

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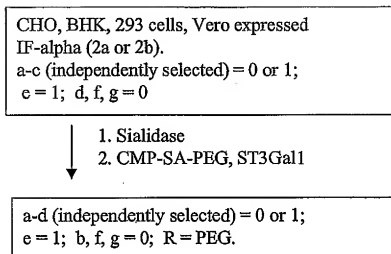


FIG. 28P

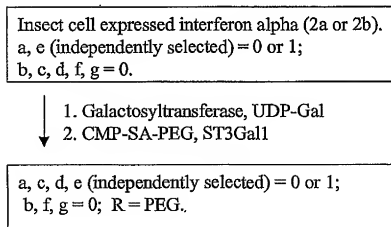


FIG. 28Q

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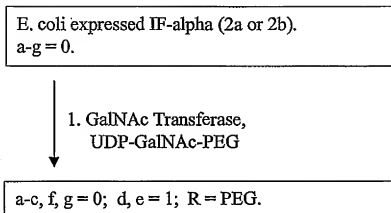


FIG. 28R

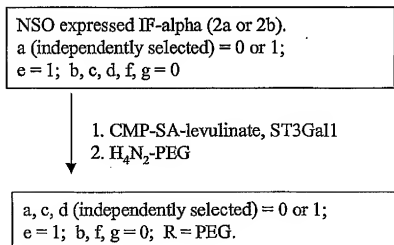


FIG. 28S

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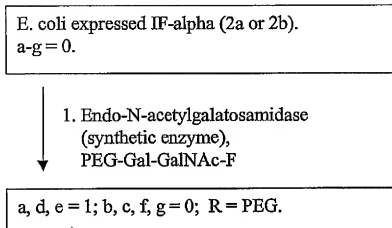


FIG. 28T

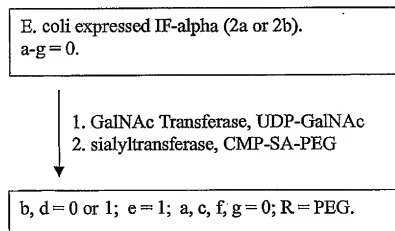


FIG. 28U



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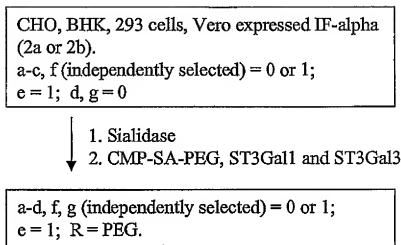


FIG. 28V

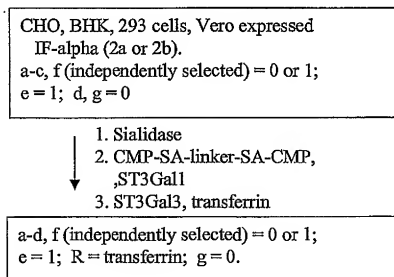


FIG. 28W



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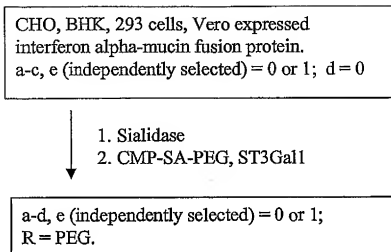


FIG. 28Y

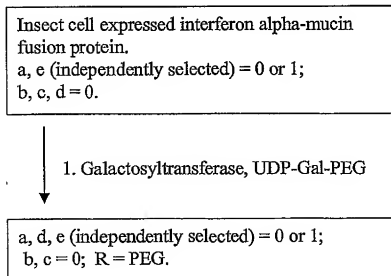


FIG. 28Z

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E. coli expressed interferon alpha-mucin  
fusion protein.  
a-c = 0.

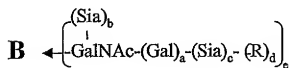
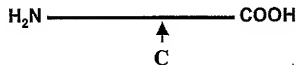
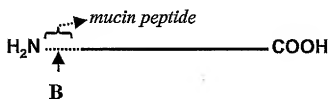
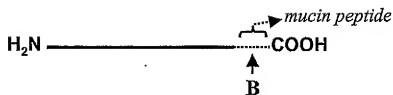


1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;  
a, b = 0; R = PEG.

FIG. 28AA

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 28BB

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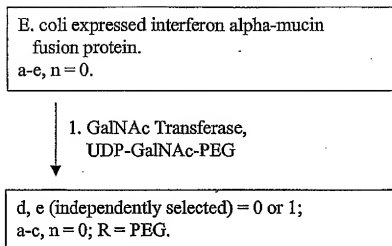


FIG. 28CC

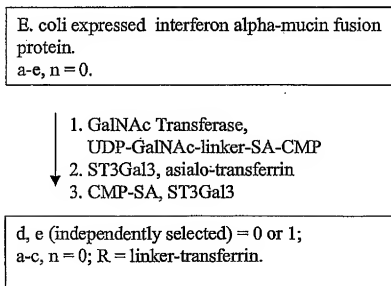


FIG. 28DD

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E. coli expressed Interferon alpha (no fusion).  
a-e, n = 0.

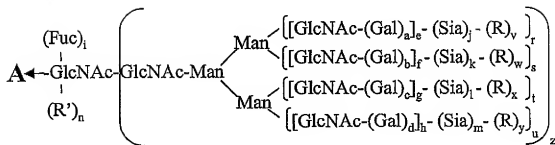


1. NHS-CO-linker-SA-CMP
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 28EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 29A



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CHO, BHK, 293 cells, Vero expressed IF-beta  
 h = 1 to 3;  
 a-g, j-m, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;  
 a-g, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 29B

Insect cell expressed IF-beta  
 a-d, f, h, j-n, s, u, v-y = 0;  
 e, g, i, r, t (independently selected) = 0 or 1;  
 z = 1.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3,  
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 j, l, v, x (independently selected) = 0 or 1;  
 z = 1; R = PEG.

FIG. 29C

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Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 29D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 29E

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Insect cell expressed IF-beta

a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t  
(independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 29F

Yeast expressed IF-beta

a-n = 0; z = 1;  
r-y (independently selected) = 0 to 1;  
R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
  2. GNT's 1,2,4,5, UDP-GlcNAc
  3. Galactosyltransferase, UDP-Gal
  - 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 29G

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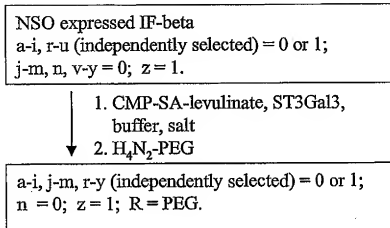


FIG. 29H

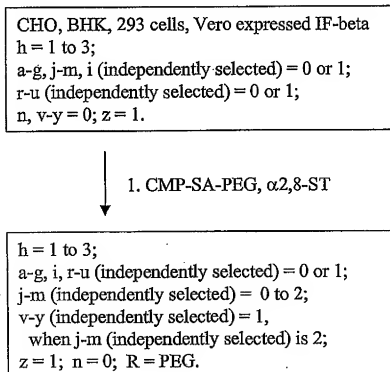


FIG. 29I

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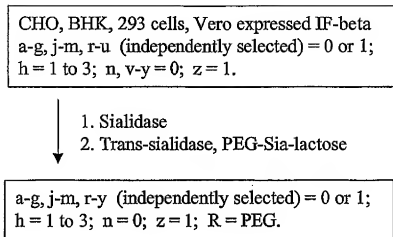


FIG. 29J

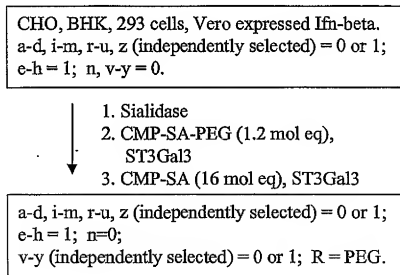


FIG. 29K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

FIG. 29L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 29M

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CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, r-u, z (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, r-u, z (independently selected) = 0 or 1;  
e-h = 1; n = 0;  
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 29N

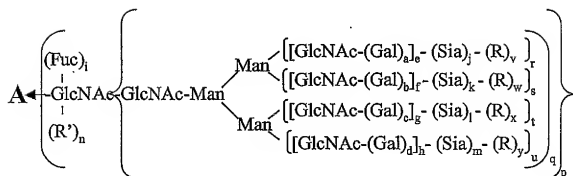
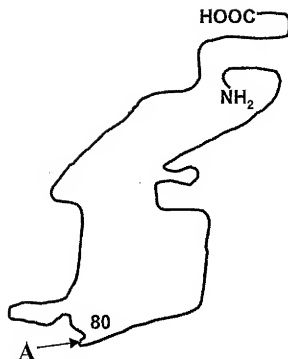
CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, r-u, z (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, r-u, z (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
n, v-y (independently selected) = 0.

FIG. 29O

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,  
glycoconjugate.

FIG. 29P



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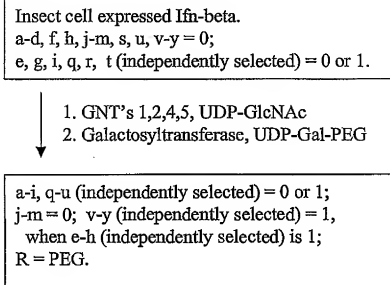


FIG. 29Q

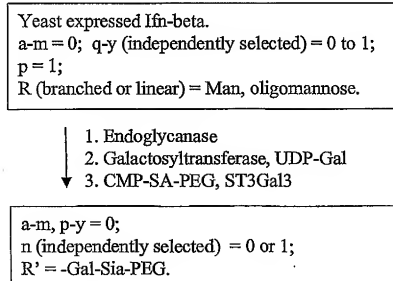


FIG. 29R

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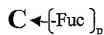
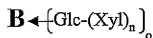
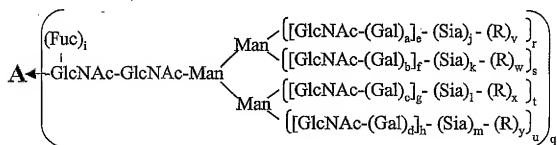
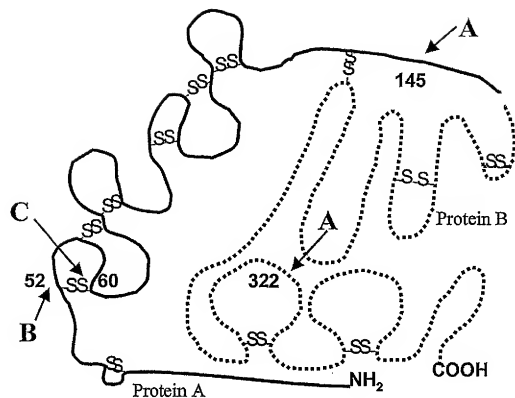
CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 29S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A.

FIG. 30A

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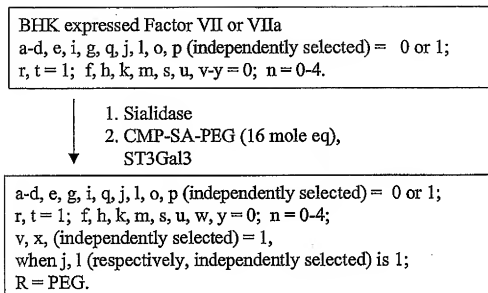


FIG. 30B

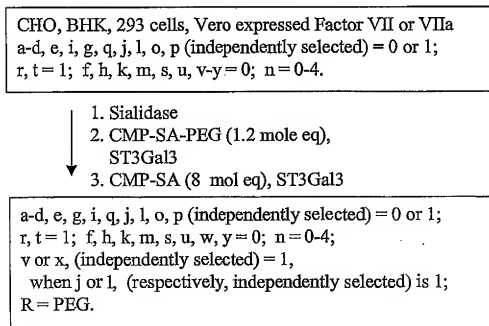


FIG. 30C

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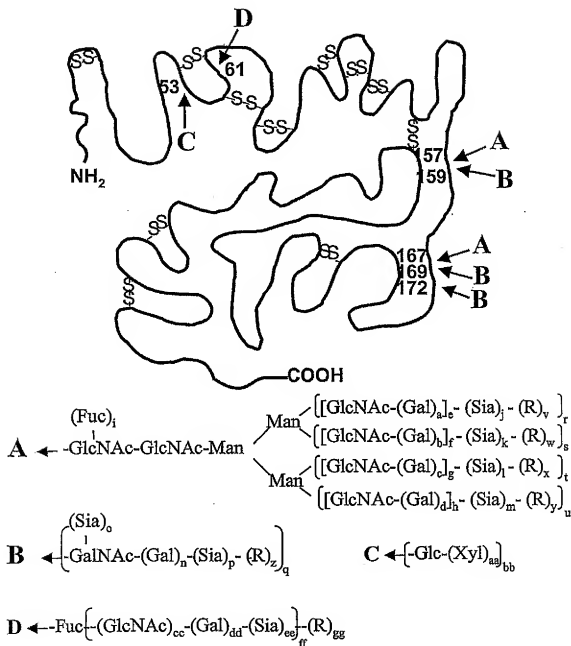
NSO expressed Factor VII or VIIa  
a--u (independently selected) = 0 or 1;  
v-y = 0; n = 0-4;  
Sia (independently selected) = Sia or Gal.

- ↓  
1. Sialidase and  $\alpha$ -galactosidase  
2. Galactosyltransferase, UDP-Gal  
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;  
n = 0-4; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
Sia = Sia; R = PEG.

FIG. 30D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 31A

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CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1;  
 R = PEG.

FIG. 31B

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3
  3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =  
 0 or 1;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1;  
 o, z = 0; R = PEG.

FIG. 31C

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CHO, BHK, 293 cells, Vero expressed Factor IX

a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i, o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;

aa, bb, cc, dd, ee, ff, i, r-u (independently selected) = 0 or 1; R = PEG;

o, v-y, gg = 0;

j-m, p, ee (independently selected) = 0 or 1, but when p = 1, z = 1.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed Factor IX

a-d, q = 1; e-h = 1 to 4;

aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently selected) = 0 or 1;

v-z, gg = 0.

- CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;

aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected) = 0 or 1; R = PEG;

o, p, z = 0; j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 31E



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CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0; R = PEG;  
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 31F

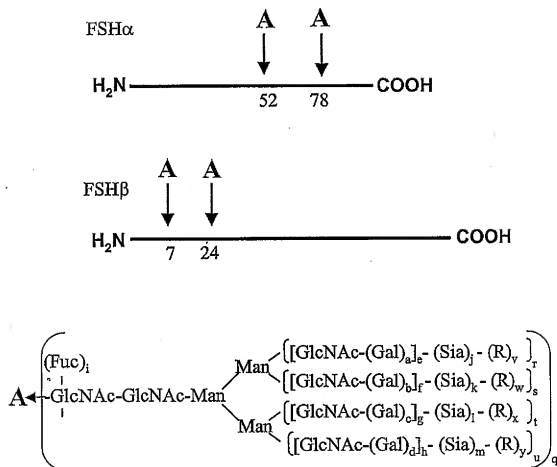
CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q, bb, cc, dd, ff = 1;  
 e-h, aa = 1 to 4;  
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α2,8-ST

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1;  
 o, p, z = 0; R = PEG;  
 j-m, ee (independently selected) = 0 to 2;  
 v-y, gg (independently selected) = 1, when j-m  
 (independently selected) is 2;

FIG. 31G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 32A

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CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 32C

104/345

NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal1

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 32D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 32E

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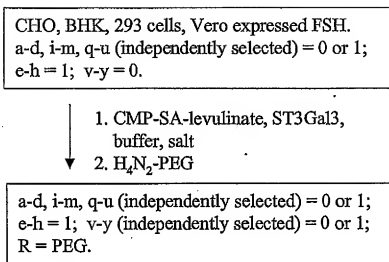


FIG. 32F

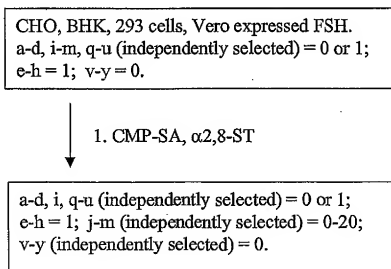


FIG. 32G

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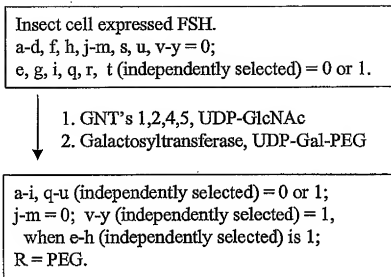


FIG. 32H

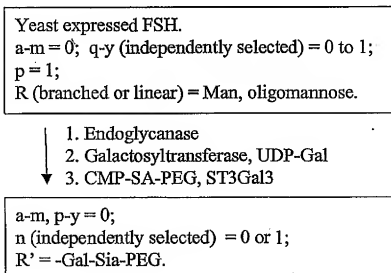


FIG. 32I

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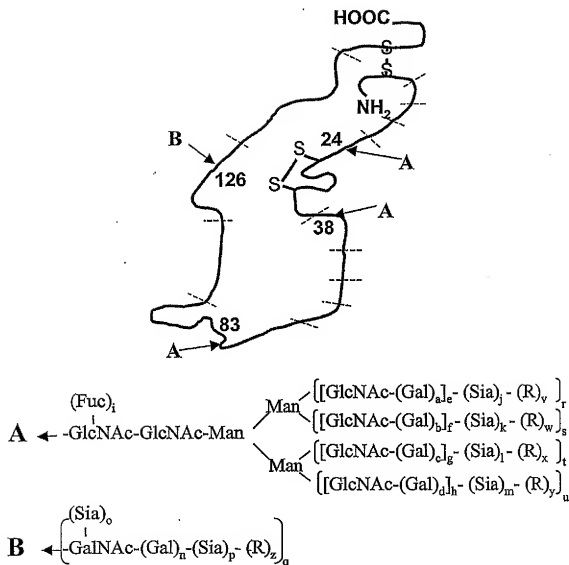
CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-CG.

FIG. 32J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 33A



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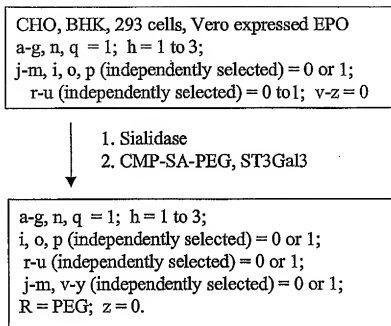


FIG. 33B

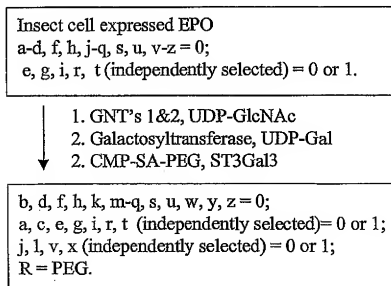


FIG. 33C

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CHO, BHK, 293 cells, Vero expressed EPO  
 a-q, r-u (independently selected) = 0 or 1;  
 v-z = 0.

- ↓
1. sialidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA, ST3Gal3
  4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;  
 i-m, o, r-u (independently selected) = 0 or 1;  
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed EPO  
 a-g, n, q = 1; h = 1 to 3;  
 j-m, i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 v-z = 0

- ↓
1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;  
 i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 R = PEG; z = 0.

FIG. 33E

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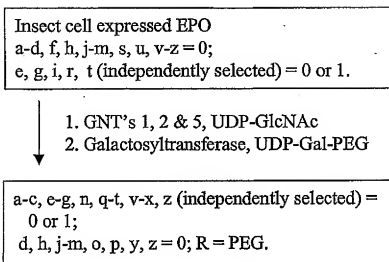


FIG. 33F

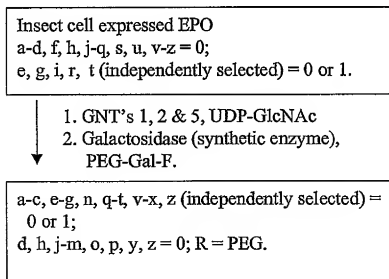


FIG. 33G

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NSO expressed NESP

q = 1; a-i, n, r-u (independently selected) = 0  
or 1; j-m, o, p, v-z = 0

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

q = 1; a-i, j-n, r-y (independently selected) =  
0 or 1;  
o, p, z = 0; R = PEG.

FIG. 33H

CHO, BHK, 293 cells, Vero expressed NESP

a-g, n, q = 1; h = 1 to 3;  
j-m, i, o, p (independently selected) = 0 or 1;  
r-u (independently selected) = 0 or 1;  
v-z = 0

- ↓
1. CMP-SA-PEG,  $\alpha$ 2,8-ST

a-g, n, q = 1; h = 1 to 3;  
i, o, p (independently selected) = 0 or 1;  
r-u (independently selected) = 0 to 1;  
j-m (independently selected) = 0 to 2;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 2;  
R = PEG; z = 0.

FIG. 33I

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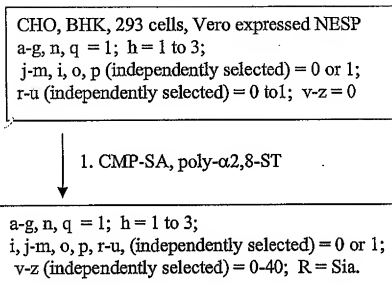
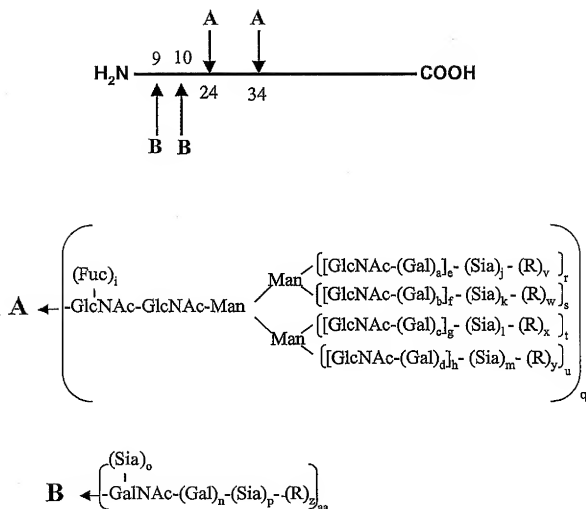


FIG. 33J

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 34A

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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
 o, p, z = 0; n, e-h = 1;  
 v-y (independently selected) = 1,  
 when j-m (independently selected) is 1;  
 R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3 &  
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;  
 o, z = 0; n, e-h = 1;  
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 34C

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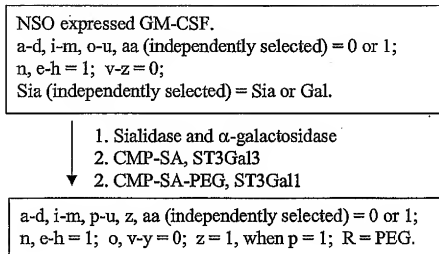


FIG. 34D

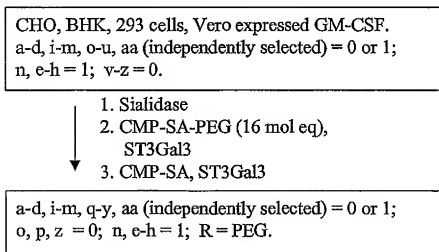


FIG. 34E



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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;  
z = 0; n, e-h = 1; R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed GMCSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

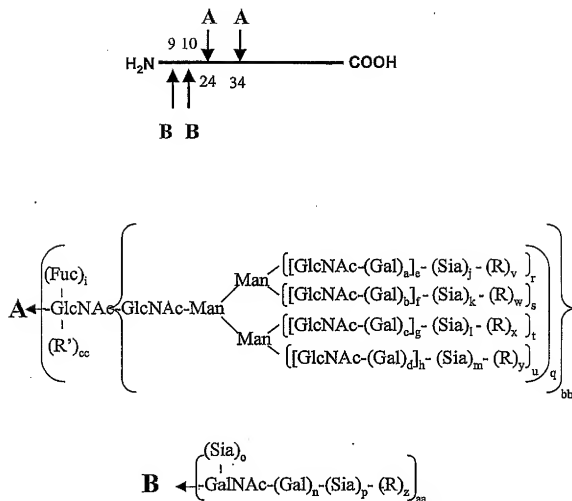


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; j-m (independently selected) = 0-20;  
v-z (independently selected) = 0.

FIG. 34G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 34H

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 34I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1. Endoglycanase
  2. mannosidase (if aa = 1).
  3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 34J

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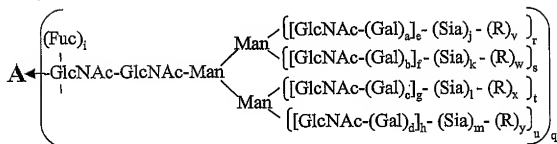
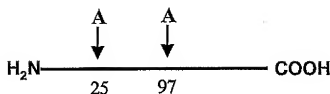
CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a--m, o-u, aa, bb (independently selected) = 0 or 1;  
n, v-z, cc = 0.

- ↓
1. sialidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-linker-SA-CMP, ST3Gal1
  3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 34K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 35A

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CHO, BHK, 293 cells, Vero expressed IF-gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 35B

CHO, BHK, 293 cells, Vero expressed IF-gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 35C

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NSO expressed Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed  
Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3
- ↓

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 35E

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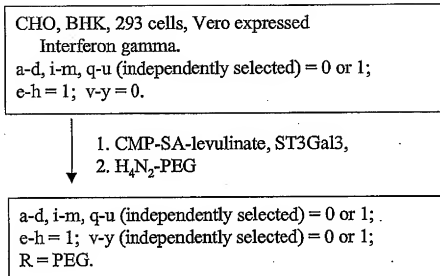


FIG. 35F

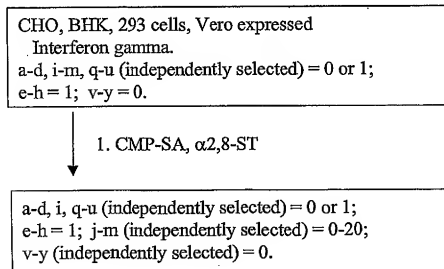
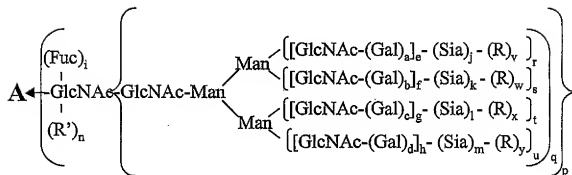
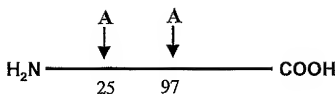


FIG. 35G



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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 35H

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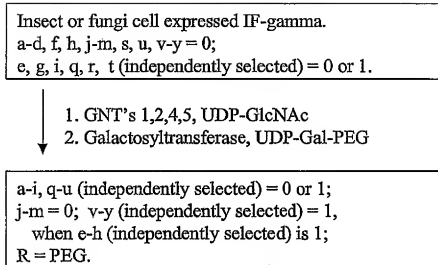


FIG. 35I

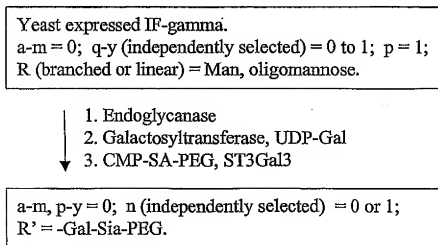


FIG. 35J

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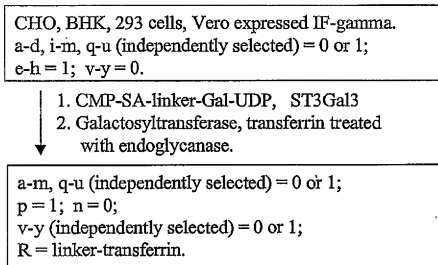


FIG. 35K

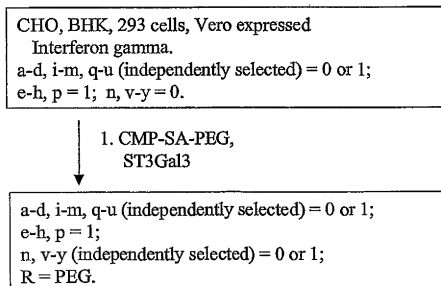


FIG. 35L

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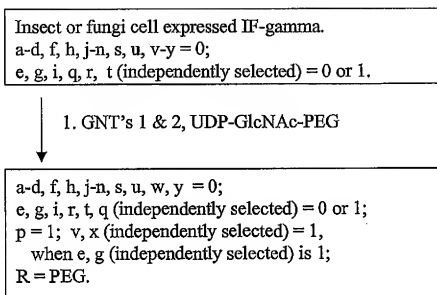


FIG. 35M

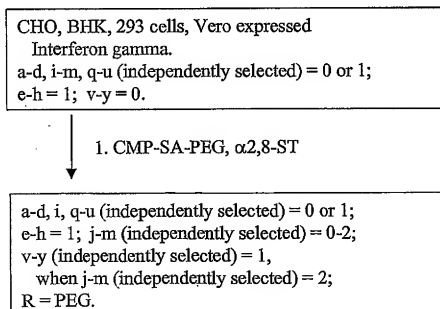
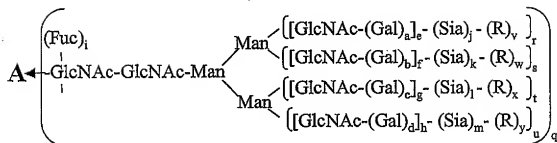
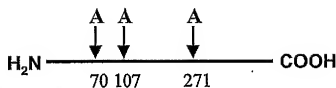


FIG. 35N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 36A

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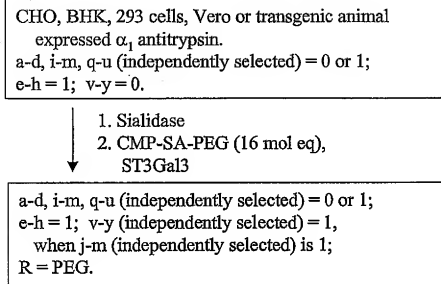


FIG. 36B

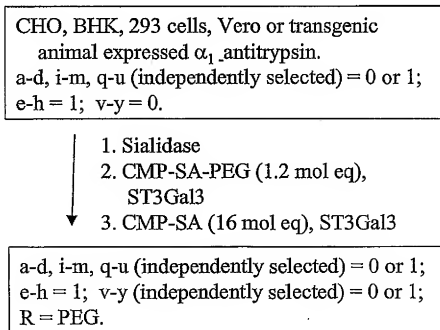


FIG. 36C

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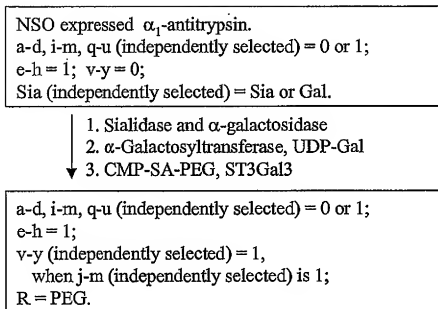


FIG. 36D

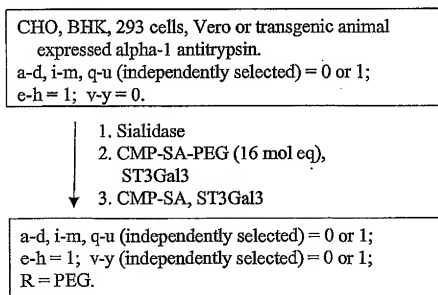


FIG. 36E

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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2.  $H_4N_2$ -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

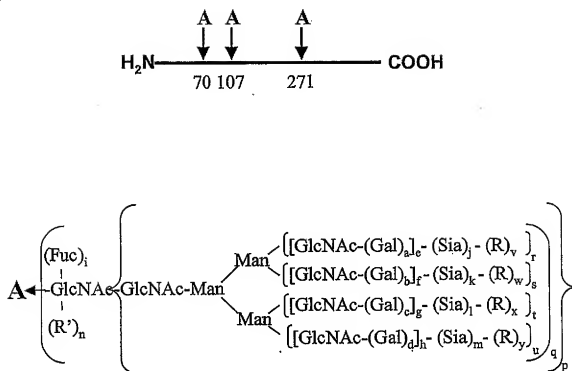
- ↓
1. CMP-SA,  $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1; e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 36G



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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

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Insect or fungi cell expressed  $\alpha_1$ -antitrypsin.  
 a-d, f, h, j-m, s, u, v-y = 0;  
 e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-m = 0;  
 v-y (independently selected) = 1,  
 when e-h (independently selected) is 1;  
 R = PEG.

FIG. 36I

Yeast expressed  $\alpha_1$ -antitrypsin.  
 a-m = 0; q-y (independently selected) = 0 to 1;  
 p = 1; R (branched or linear) = Man, oligomannose.

- ↓
1. Endoglycanase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;  
 R' = -Gal-Sia-PEG.

FIG. 36J

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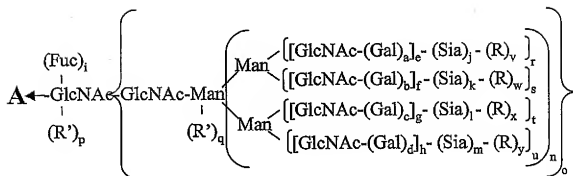
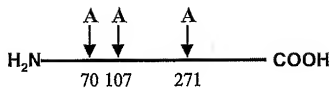
CHO, BHK, 293 cells, Vero expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin treated  
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 36K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 36L

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Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

- ↓ 1. endoglycanase  
 ↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 36M

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n = 1; R' = xylose

- ↓ 1. hexosaminidase,  
 2. alpha mannosidase and xylosidase  
 ↓ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 36N

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CHO, BHK, 293 cells, Vero, transgenic animal  
expressed  $\alpha_1$  antitrypsin.  
a-h, i-o, r-u (independently selected) = 0 or 1;  
p, q, v-y = 0.

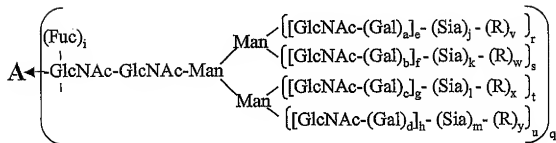
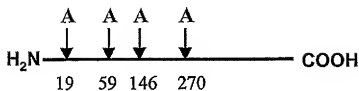


1. CMP-SA-PEG,  
ST3Gal3

a-h, i-o, r-u (independently selected) = 0 or 1;  
p, q = 0; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 360

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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CHO, BHK, 293 cells, Vero expressed Cerezyme  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 37B

CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-M-6-P (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = mannose-6-phosphate

FIG. 37C



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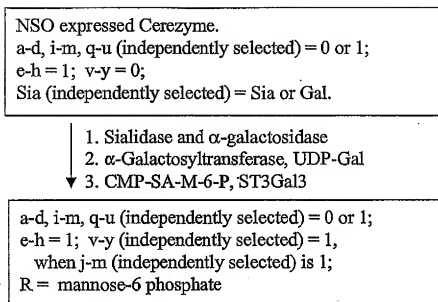


FIG. 37D

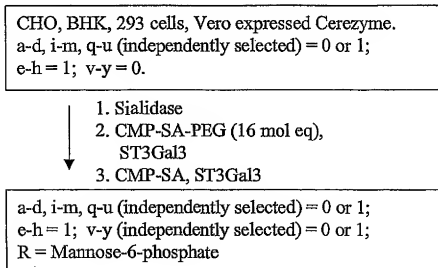


FIG. 37E

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CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt.
  2. H<sub>4</sub>N<sub>2</sub>-spacer-M-6-P or clustered M-6-P

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = M-6-P or clustered M-6-P

FIG. 37F

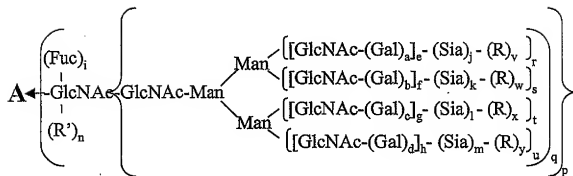
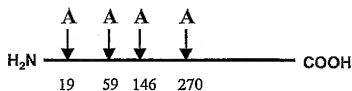
CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 37G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 37H

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Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 37I

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 37J

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CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

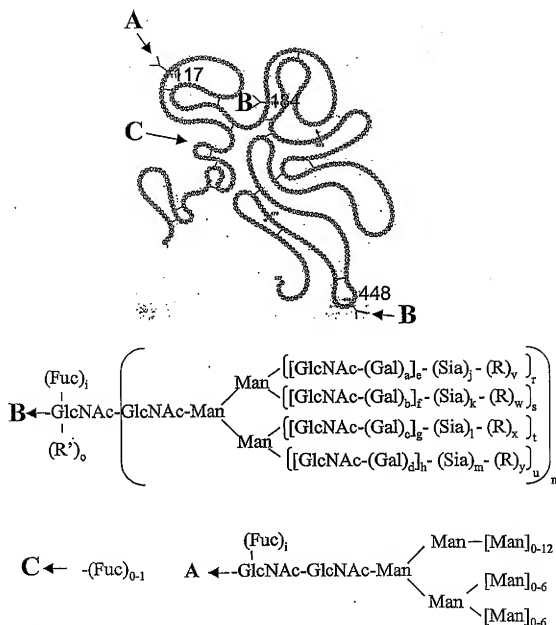


1. CMP-SA-linker-SA-CMP,  
ST3Gal3
2. ST3Gal3, desialylated transferrin.
3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0; v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 37K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 38A

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CHO, BHK, 293 cells, Vero expressed tPA  
 a-g, n = 1; h = 1 to 3;  
 j-m, i, (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;  
 i, r-u (independently selected) = 0 or 1;  
 o = 0; j-m, v-y (independently selected) = 0 or 1;  
 R = PEG

FIG. 38B

Insect or fungi cell expressed tPA  
 A = B; a-d, f, h, j-o, s, u, v-y = 0;  
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 n = 1; j, l, v, x (independently selected) = 0 or 1;  
 R = PEG.

FIG. 38C

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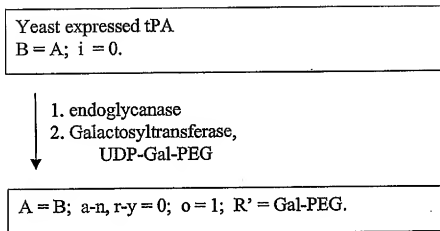


FIG. 38D

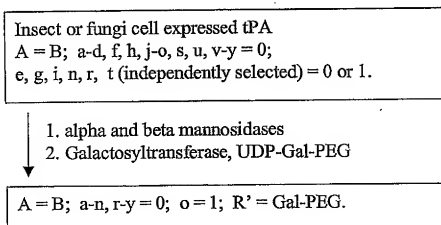


FIG. 38E



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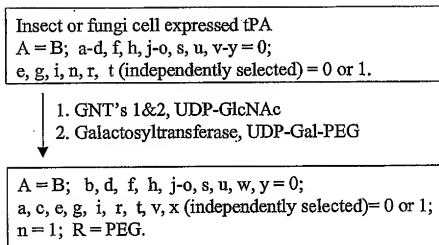


FIG. 38F

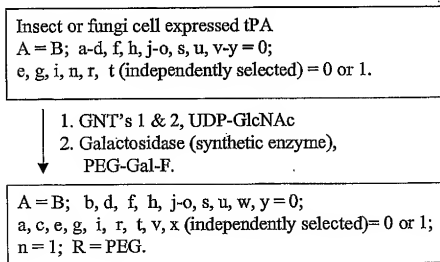
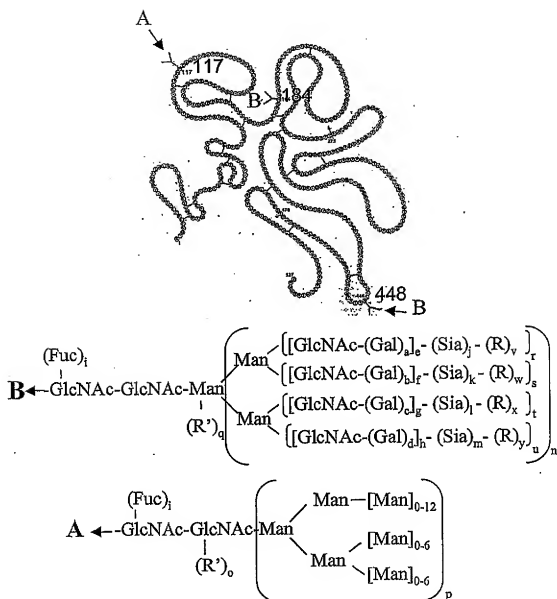


FIG. 38G

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 38H

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NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;  
 n = 1; o, p, q, v-y = 0

1. sialidase, alpha-galactosidase
2. CMP-SA-levulinate, ST3Gal3,
3. H<sub>4</sub>N<sub>2</sub>-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;  
 n = 1; o, p, q = 0;  
 v-y (independently selected) = 1,  
 when j-m (independently selected) is 1;  
 R = PEG.

FIG. 38I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;  
 j-m, i, (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1; q, o, v-y = 0.

1. alpha and beta Mannosidases
2. CMP-SA, ST3Gal3
3. Galactosyltransferase, UDP-Gal-PEG


a-g, n = 1; h = 1 to 3;  
 i, r-u (independently selected) = 0 or 1; o = 1;  
 q, p, v-y = 0; j-m (independently selected) = 0 or 1;  
 R' = Gal-PEG

FIG. 38J

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Plant expressed tPA

A = B; a-d, f, h, j- m, s, u, v-y = 0;  
e, g, i, q, r, t (independently selected) = 0 or 1;  
n = 1; R' = xylose

- 
1. hexosaminidase,
  2. alpha mannosidase and  
xylosidase
  3. GlcNAc transferase, UDP-  
GlcNAc-PEG

A = B; a-d, f, h, j-n, s, u, v-y = 0;  
e, g, i, r, t (independently selected) = 0;  
q = 1; R' = GlcNAc-PEG.

FIG. 38K



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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 38M

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

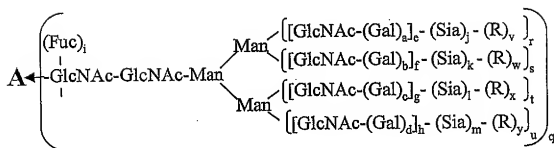
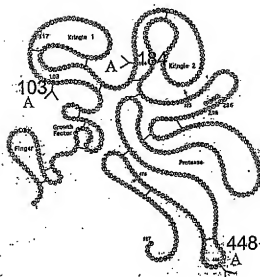
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 380

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38P



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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38Q

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2.  $H_4N_2$ -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 38R

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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 38S



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Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 38U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 38V

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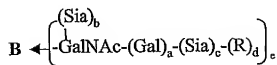
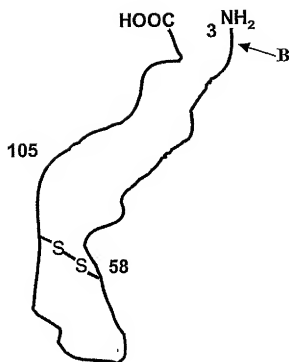
CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, anti-TNF  
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;  
n = 0; v-y (independently selected) = 0 or 1;  
R = linker-anti-TNF IG chimera protein.

FIG. 38W

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a-c, e (independently selected) = 0 or 1;  
 d = 0;  
 R = modifying group, mannose, oligo-  
 mannose.

FIG. 39A

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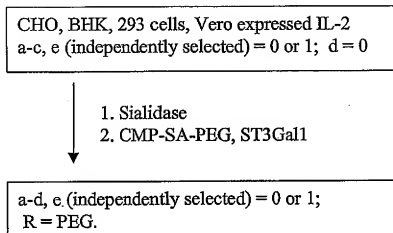


FIG. 39B

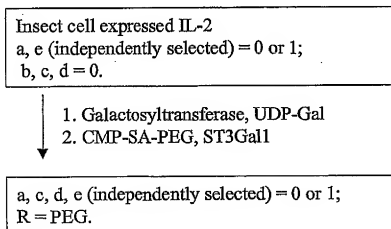


FIG. 39C

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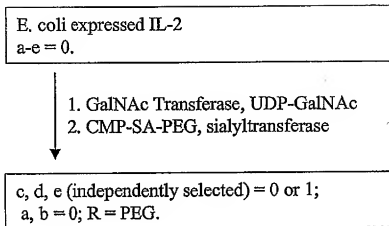


FIG. 39D

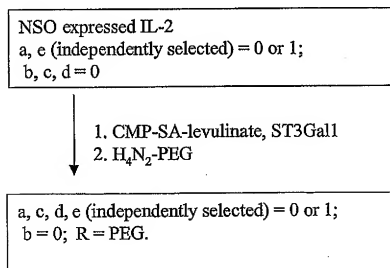


FIG. 39E



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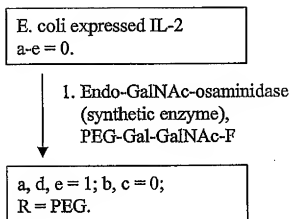


FIG. 39F

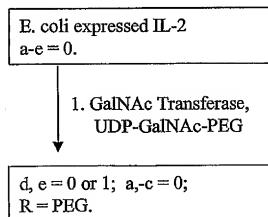
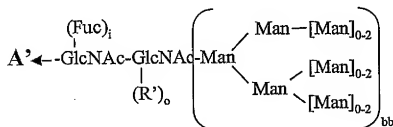
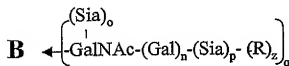
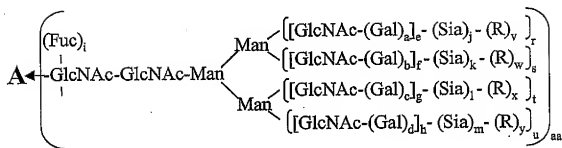


FIG. 39G

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2 peptides  
 A and A' - N-linked sites  
 B - O-linked sites



Alternate structure  
 for some N-linked  
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.

aa, bb (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer, glycoconjugate.

FIG. 40A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed  
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3
  3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40C

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CHO, BHK, 293s cells, Vero, MDCK, HEKC  
expressed Factor VIII.  
e-h = 1 to 4;  
aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;  
v-z = 0.

↓  
1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;  
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;  
z = 0; j-m, v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40D

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.  
e-h = 1 to 4;  
aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;  
v-z = 0.

↓  
1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;  
aa, bb, a-d, i, n-u (independently selected) = 0 or 1;  
z = 0; j-m, v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG,  $\alpha$ 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

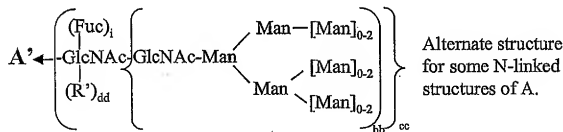
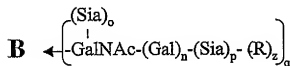
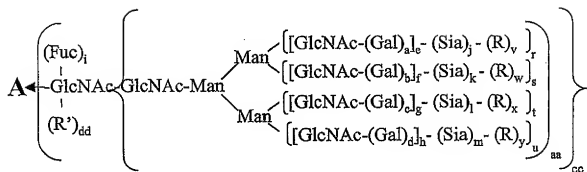
when j-m (independently selected) is 2;

R = PEG.

FIG. 40F

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2 peptides

**A or A'** - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 40G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓  
1. CMP-SA-levulinate, ST3Gal3,  
2.  $H_4N_2$ -PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40H

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓  
1. endo-H  
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
  2. endo-H
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40J

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT 1 & 2, UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 40K



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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT-1, 2, 4 & 5; UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal
  4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 40L

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT-1, UDP-GlcNAc-PEG

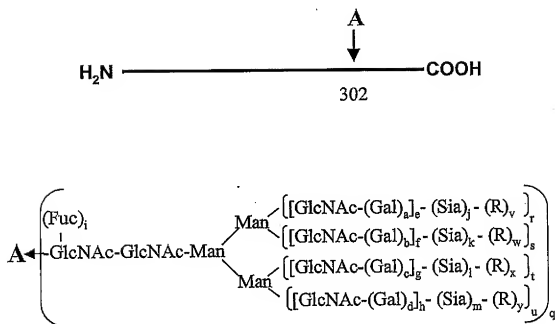
e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 40M

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a-d, i, q-u (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 100.  
 v-y = 0; R = polymer.

FIG. 41A

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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 41B

CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 41C

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NSO expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 41D

CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 41E

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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 41F

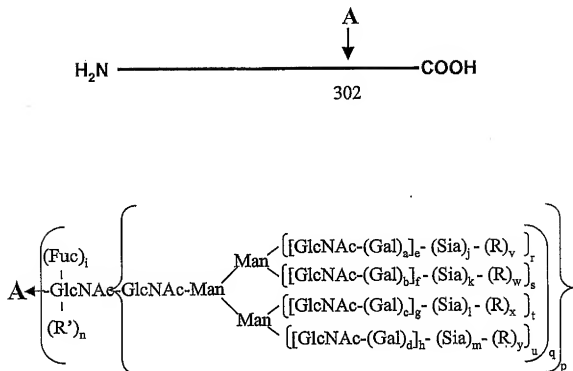
CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 41G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 41H

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Insect cell expressed Urokinase.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-n = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 41I

Yeast expressed Urokinase.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 41J

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CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

↓ 1. CMP-SA-linker-SA-CMP, ST3Gal3

2. ST3Gal1, desialylated Urokinase produced in CHO.

↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 41K

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

↓ 1. sulfohydrolase

2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 41L



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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

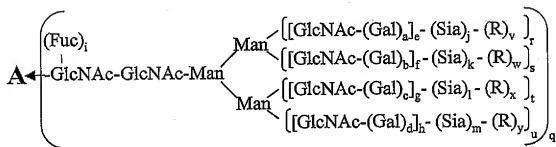
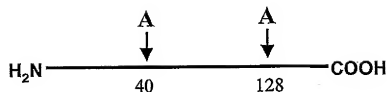
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 41M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 42B

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 42C

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NSO expressed DNase I.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 42D

CHO, BHK, 293 cells, Vero expressed DNase I.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq), ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42E

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 42F

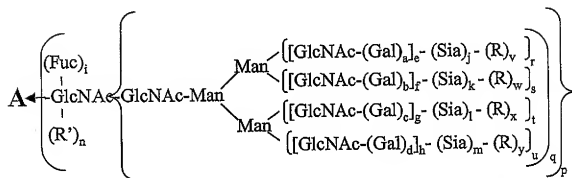
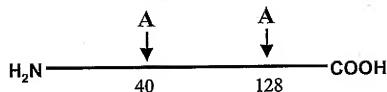
CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 42G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 42H

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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 42I

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 42J

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.

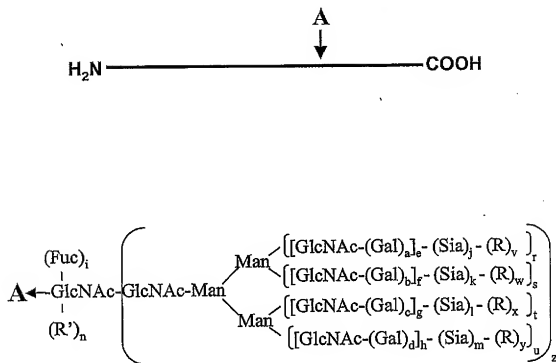
- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker- alpha-1-Proteinase inhibitor.

FIG. 42K



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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 43A

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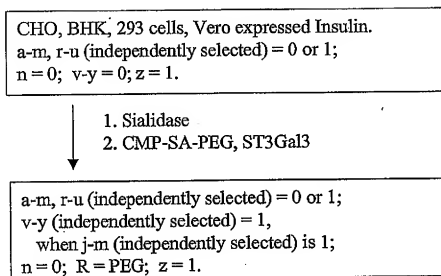


FIG. 43B

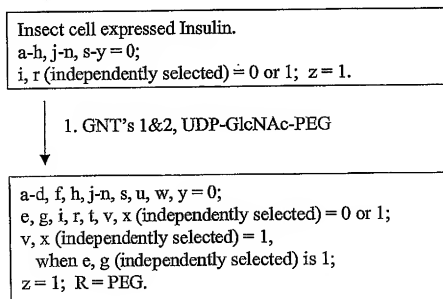


FIG. 43C

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Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or  
polysaccharide.



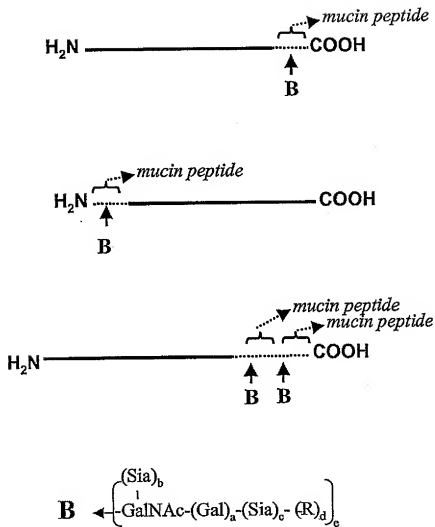
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 43D

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = polymer

FIG. 43E

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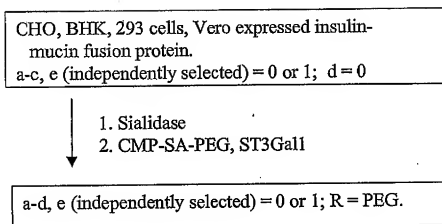


FIG. 43F

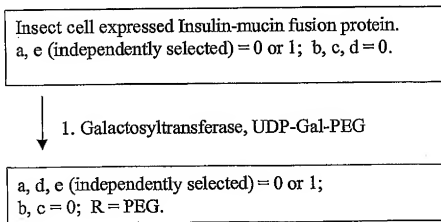


FIG. 43G

194/345

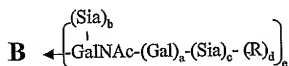
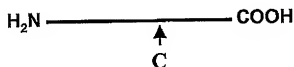
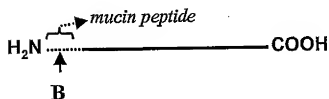
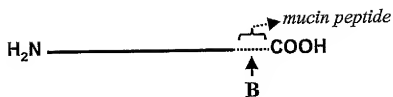
E. coli expressed Insulin-mucin fusion protein.  
a-e = 0.

- ↓
1. GalNAc Transferase, UDP-GalNAc
  2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;  
a, b = 0; R = PEG.

FIG. 43H

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = modifying group, mannose,  
 oligo-mannose.

FIG. 43I

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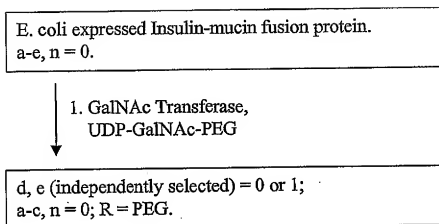


FIG. 43J

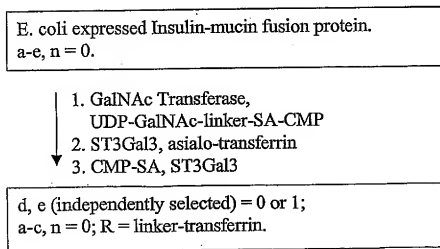


FIG. 43K



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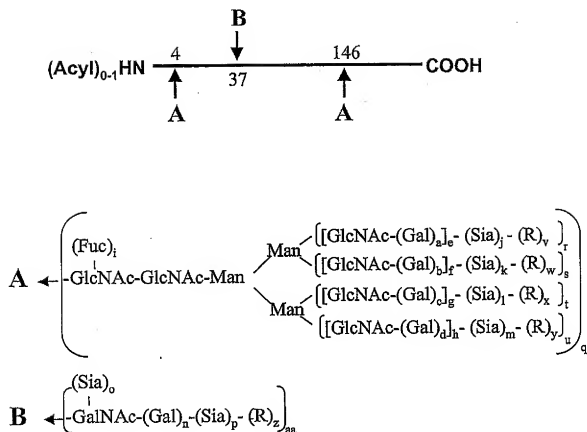
*E. coli* expressed Insulin (N)—no mucin peptide.  
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  3. CMP-SA, ST3Gal3

a-e = 0; n = 1;  
R' = linker-transferrin.

FIG. 43L

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

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CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-linker-lipid-A,  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = linker-lipid-A.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
  2. CMP-SA-linker-tetanus toxin, ST3Gal1
  3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 44C

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NSO expressed M-antigen.

a-d, i-n, o-u, aa (independently selected) = 0 or 1;

e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1.  $\alpha$ -galactosidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-KLH, ST3Gal1

a-d, i-n, p-u, z, aa (independently selected) = 0 or 1;

e-h = 1; o, v-y = 0;

z = 1, when p = 1;

R = KLH.

FIG. 44D

Yeast expressed M-antigen.

a-p, z = 0; q-y, aa (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1.  $\alpha$ 1,2-mannosidase
  2. GNT 1,
- ↓ UDP-GlcNAc-linker-diphtheria toxin.

e, q, l, m, r, t, u, v, aa (independently selected) = 0 or 1;

a-d, f-h, j, k, n-p, s, w-z = 0;

Sia = Man; R = linker-diphtheria toxin.

FIG. 44E

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CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
2. H<sub>4</sub>N<sub>2</sub>-linker-DNA

a-d, i-m, o-y, aa (independently selected) = 0 or 1;  
z = 0; n, e-h = 1; R = linker-DNA.

FIG. 44F

CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-n, o-u, aa (independently selected) = 0 or 1;  
e-h = 1; v-z = 0.

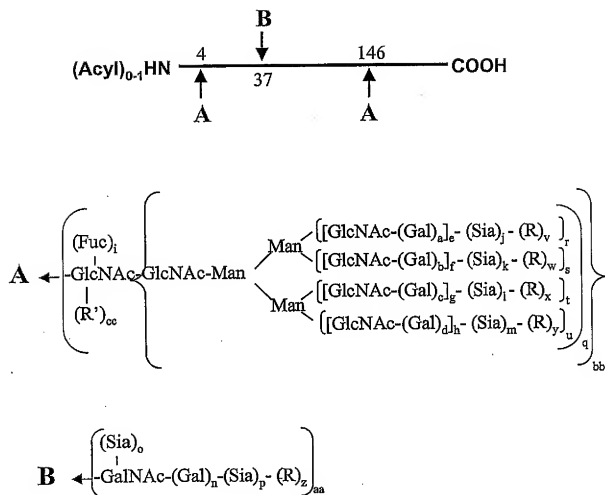


1. CMP-SA, poly- $\alpha$ 2,8-ST

a-d, i, n-u, aa (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-100;  
v-z (independently selected) = 0.

FIG. 44G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-p (independently selected) = 0 to 100.  
 Cc, v-y = 0;  
 R = modifying group, mannose, oligo-mannose.  
 R' = H, glycosyl residue, modifying group,  
 glycoconjugate.

FIG. 44H

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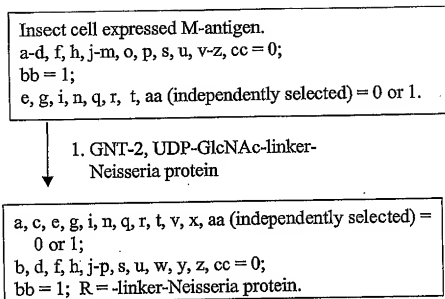


FIG. 44I

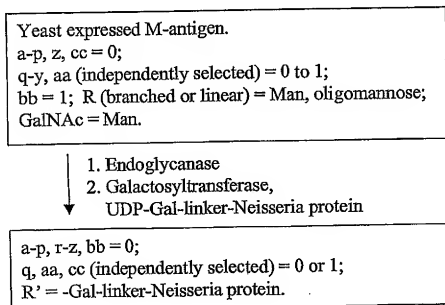


FIG. 44J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

4. CMP-SA, sialyltransferase

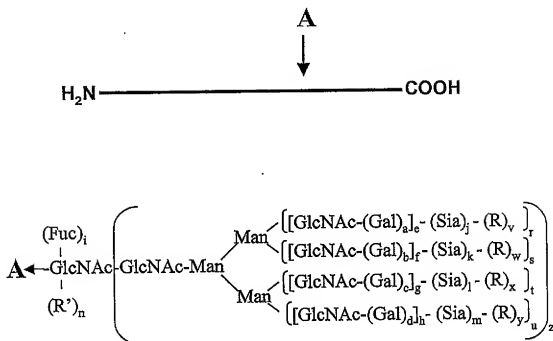
a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 44K



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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 45A

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CHO, BHK, 293 cells, Vero expressed Growth Hormone.

a-m, r-u (independently selected) = 0 or 1;  
n = 0; v-y = 0; z = 1.

1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
n = 0; R = PEG; z = 1.

FIG. 45B

Insect cell expressed growth hormone.

a-h, j-n, s-y = 0;  
i, r (independently selected) = 0 or 1; z = 1.

1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;  
e, g, i, r, t, v, x (independently selected) = 0 or 1;  
v, x (independently selected) = 1,  
when e, g (independently selected) is 1;  
z = 1; R = PEG.

FIG. 45C

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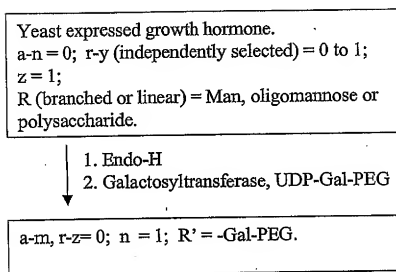
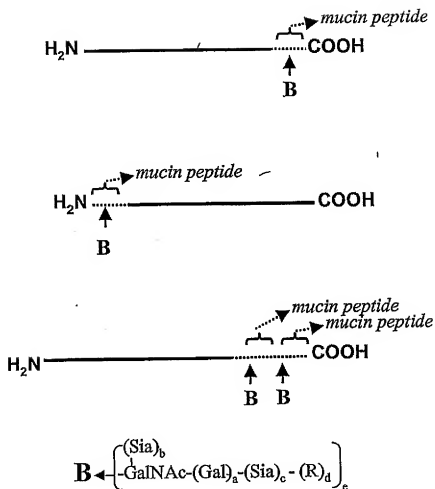


FIG. 45D

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a-c, e (independently selected) = 0 or 1;  
 d = 0;  
 R = modifying group, mannose, oligo-  
 mannose.

FIG. 45E

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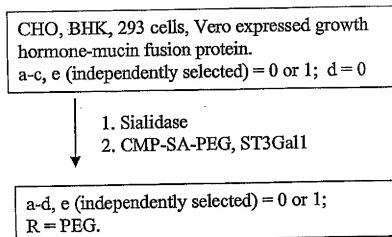


FIG. 45F

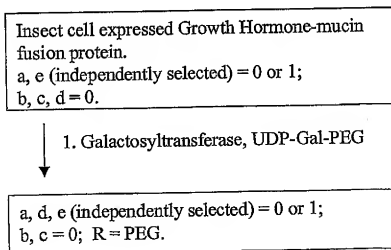


FIG. 45G

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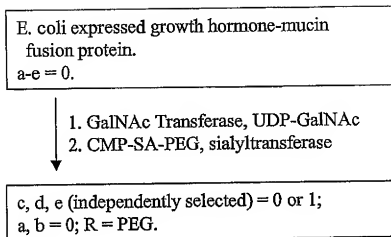


FIG. 45H

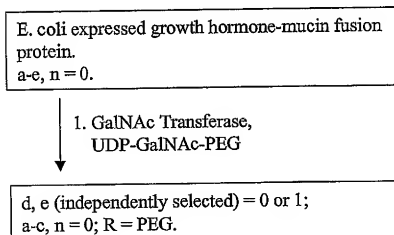


FIG. 45I

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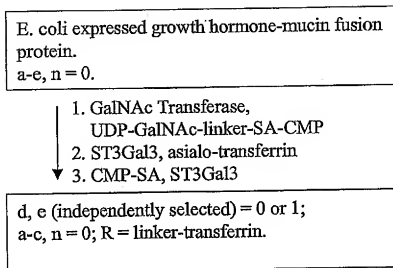


FIG. 45J

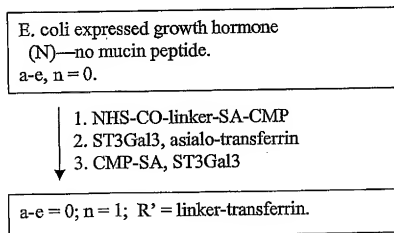
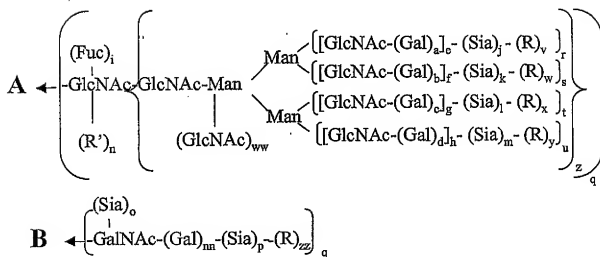
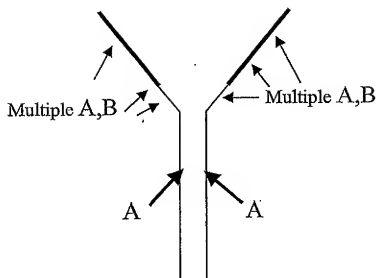


FIG. 45K

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a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46A



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CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.  
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
  2. galactosyltransferase, UPD-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.  
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. sialidase
  2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;  
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 46C

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CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.  
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.



1. galactosyltransferase, UPD-Gal-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 46D

CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.  
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.



1. CMP-SA, ST3Gal1

2. galactosyltransferase, UPD-Gal-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 46E

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CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal1
  2.  $H_4N_2$ -PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 46F

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.

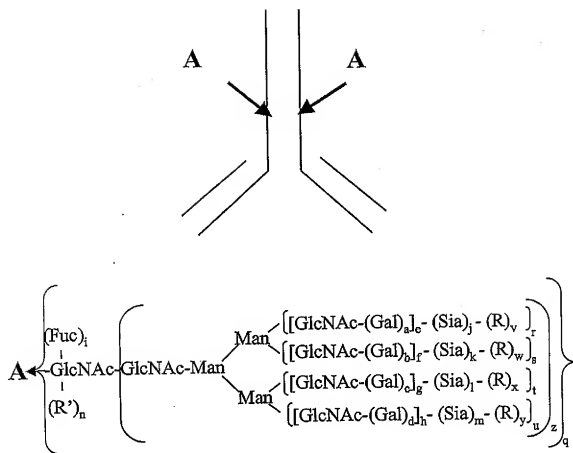
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. CMP-SA-PEG,  $\alpha 2,8$ -ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;  
n = 1; j-m, p (independently selected) = 0 to 2;  
v-z (independently selected) = 1,  
when j-m, p (independently selected) is 2;  
R = PEG.

FIG. 46G

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a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-k (independently selected) = 0 or 1.

M = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 47A

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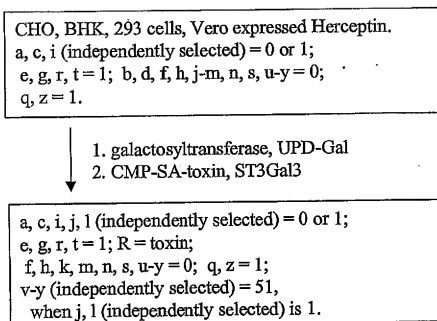


FIG. 47B

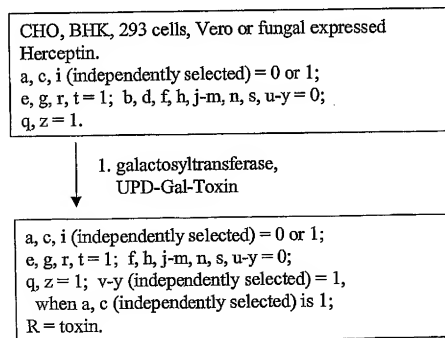


FIG. 47C

218/345

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

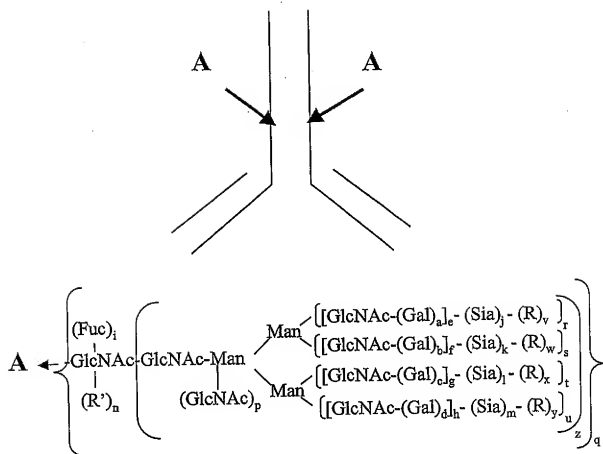
1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ↓ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 47D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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CHO, BHK, 293 cells, Vero expressed Synagis.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1;  
 b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
  2. CMP-SA-PEG, ST3Gal3

a, c, i, j, w, (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when j, l (independently selected) is 1;  
 R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero or fungal expressed  
 Synagis.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.

- ↓
1. galactosyltransferase,  
 UPD-Gal-PEG

a, c, i, w (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when a, c (independently selected) is 1;  
 R = PEG.

FIG. 48C



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Fungi expressed Synagis.

e, g, i, r, t (independently selected) = 0 or 1;

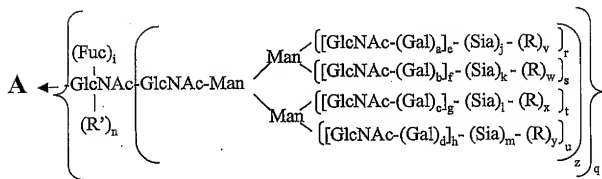
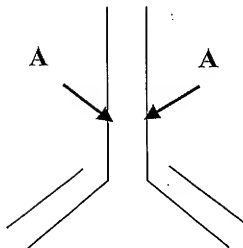
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 48D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

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CHO, BHK, 293 cells, Vero expressed Remicade.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
  2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = PEG.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Remicade.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.

- ↓
1. galactosyltransferase,  
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when a, c (independently selected) is 1;  
R = PEG.

FIG. 49C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

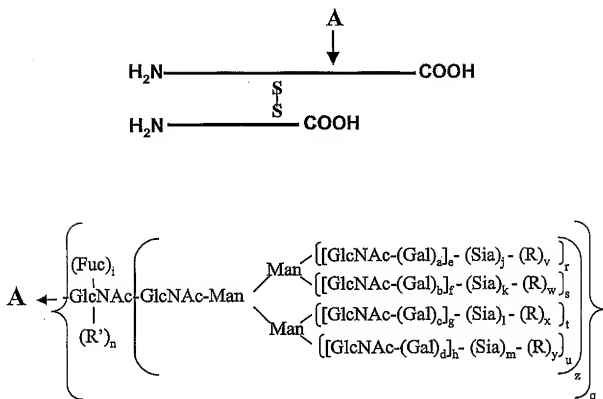
- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 50A

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CHO, BHK, 293 cells, Vero expressed Reopro.  
a-m, r-u (independently selected) = 0 or 1;  
n = 0; v-y = 0; z = 1.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
n = 0; R = PEG; z = 1.

FIG. 50B

Insect cell expressed Reopro.  
a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;  
z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;  
e, g, i, r, t, v, x (independently selected) = 0 or 1;  
v, x (independently selected) = 1,  
when e, g (independently selected) is 1;  
z = 1; R = PEG.

FIG. 50C

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Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

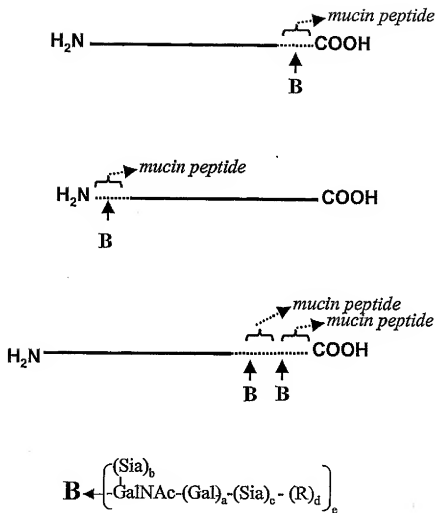
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 50D

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = polymer

FIG. 50E



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CHO, BHK, 293 cells, Vero expressed  
Reopro-mucin fusion protein.  
a-c, e (independently selected) = 0 or 1; d = 0



1. Sialidase
2. CMP-SA-PEG, ST3Gal1

a-d, e (independently selected) = 0 or 1; R = PEG.

FIG. 50F

Insect cell expressed Reopro-mucin fusion protein.  
a, e (independently selected) = 0 or 1; b, c, d = 0.



1. Galactosyltransferase, UDP-Gal-PEG

a, d, e (independently selected) = 0 or 1;  
b, c = 0; R = PEG.

FIG. 50G

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E. coli expressed Reopro-mucin fusion protein.  
a-e = 0.

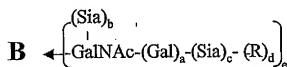
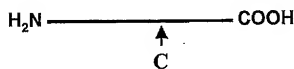
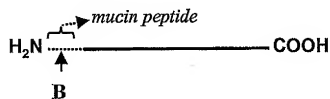
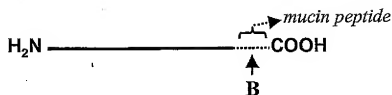


1. GalNAc Transferase, UDP-GalNAc
2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;  
a, b = 0; R = PEG.

FIG. 50H

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 50I

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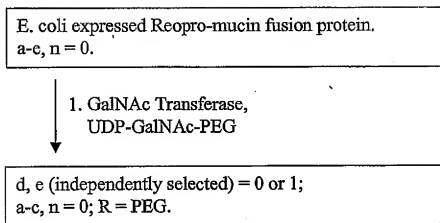


FIG. 50J

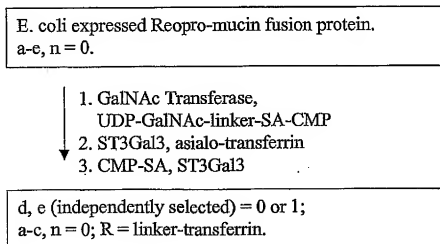


FIG. 50K

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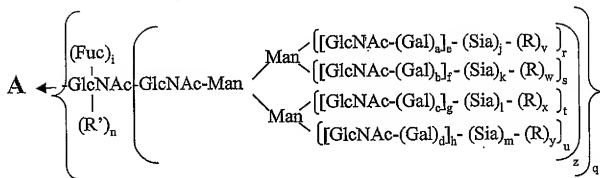
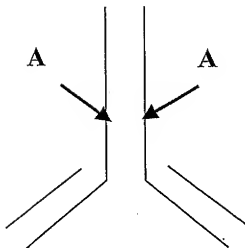
E. coli expressed Reopro(N)—no mucin peptide.  
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 50L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 51A

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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;

e, g, r, t = 1;

f, h, k, m, n, s, u-y = 0; q, z = 1;

v-y (independently selected) = 1,

when j, l (independently selected) is 1;

R = toxin.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed  
Rituxan.

a, c, e, g, i, r, t (independently selected) = 0 or 1;

b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase,  
UPD-Gal-drug

a, c, i (independently selected) = 0 or 1;

e, g, r, t = 1; f, h, j-m, n, s, u-y = 0; q, z = 1;

v-y (independently selected) = 1,

when a, c (independently selected) is 1;

R = toxin.

FIG. 51C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ↓ 3. CMP-SA-radioisotope complex, ST3Gal3

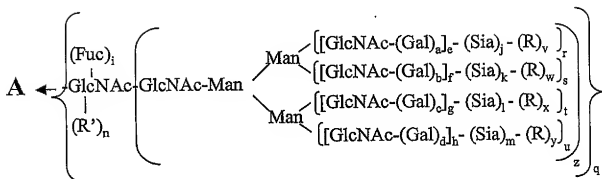
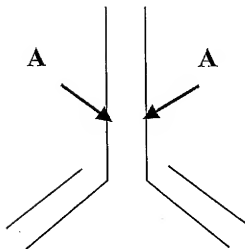
a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D



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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,  
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51E

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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
  2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = PEG.

FIG. 51F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;  
a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;  
R (independently selected) = mannose, oligomannose,  
polymannose.

- ↓
1. mannosidases (alpha and beta)
  2. GNT-I,II, UDP-GlcNAc
  3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;  
R' = -Gal-radioisotope complex.

FIG. 51G

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FIG. 52A

ACCCCCCTGGGCCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT  
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG  
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCGAGGAGCTGGT  
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGTG  
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA  
GCGGCCTTTTCTCTACCCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT  
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG  
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC  
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT  
TTCCAGCGCCGGGCAGGAGGGGTCTGTTGCCCTCCCATCTGCAGAG  
CTTCTCGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG  
A

FIG. 52B.

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr  
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro  
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe  
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro  
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val  
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
Leu Ala Gln Pro

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FIG. 53B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser  
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr  
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala  
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr  
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu  
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val  
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe  
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val  
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu  
Arg Ser Lys Glu

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FIG. 54A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC  
 ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA  
 AGCAGCAATTTTCAGTGTCTCAGAAGCTCCTGTGGCAATTGAATGGGAG  
 GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG  
 AGATTAAGCAGCTGCAGCAGTTCAGAAAGGAGGACGCCGATTGACC  
 ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA  
 TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA  
 TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC  
 TGGAGAAAGAAGATTTTACCAGGGGAAAACTCATGAGCAGTCTGCAC  
 CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA  
 GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA  
 ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT  
 CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC  
 AACCAGCAGATGCTGTTTAAAGTGACTGATGGCTAATGTACTGCAAAT  
 GAAAGGACACTAGAAGATTTTGAATTTTATTAAATTATGAGTTATT  
 TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 54B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala  
 Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly ArgLeu Glu Tyr Cys Leu Lys Asp  
 Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu  
 Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp  
 Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile  
 Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val  
 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 55A

ATGGTCTCCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG  
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCACGGCGT  
CCTGCACCGGCGCCGGCGCGCAACCGCTTCCTGGAGGAGCTGCGGC  
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA  
GGAGGCCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC  
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA  
GAATGGGGGCTCCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCT  
GCCTCCCTGCCCTTCGAGGGCCGGAACCTGTGAGACGCACAAGGATGAC  
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG  
TGACCACACGGGCACCAAGCGCTCCTGTCCGTGCCACGAGGGGTACT  
CTCTGCTGGCAGACGGGGTGTCTTGACACCCACAGTTGAATATCCA  
TGTGGA AAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA  
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA  
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC  
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA  
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC  
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG  
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACACGACATC  
GCGCTGCTCCGCTGCACACGCCCGTGGTCCTCACTGACCATGTGGTG  
CCCCCTGCGCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC  
GTGCGCTTCTCATTGGTACGCGGCTGGGGCCAGCTGCTGGACCGTGG  
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA  
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT  
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA  
CTCCTGCAAGGGGGACAGTGGAGGCCCACATGCCACCCACTACCGGG  
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA  
ACCGTGGGCCACTTTGGGGGTGTACACCAGGGTCTCCAGTACATCGA  
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCAGGAGTCTCTC  
TGCGAGCCCCATTCCC

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FIG. 55B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys  
Leu Ala Ala Val Phe Val Thr Gln Glu Ala His Gly Val Leu His Arg Arg Arg  
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg  
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys  
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val  
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg  
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro  
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys  
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln  
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile  
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg  
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp  
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu  
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser  
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu  
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg  
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp  
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg  
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly  
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met  
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 56A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC  
CATCTGCCCTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTCTT  
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA  
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT  
GTATGGAAGAAAAGTGTAGTTTGAAGAACCACGAGAAGTTTTTGAA  
AACACTGAAAAGACAACCTGAATTTGGAAGCAGTATGTTGATGGAGA  
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG  
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA  
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG  
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT  
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT  
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAAACTTCTAAGCTCAC  
CCGTGCTGAGGCTGTTTTTCTGTATGTGGACTATGTAAATCCTACTGA  
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA  
ATGACTTCACCTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA  
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA  
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTGTGCTGCCACTGTGT  
GAAACTGGTGTAAAAATTACAGTTGTGCGAGGTGAACATAATATTGA  
GGAGACAGAACATACAGAGCAAAAAGCGAAATGTGATTTCGAGCAATT  
ATTCCTCACCACAACATACAATGCAGCTATTAATAAGTACAACCATGA  
CATTGCCCTTCTGGAAGCTGGACGAACCTTATGTGCTAAACAGCTACG  
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCTCTCA  
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA  
GGGAGATCAGCTTTAGTTCCTCAGTACCTTAGAGTTCCACTTGTTGAC  
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT  
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTTCATGTCAAGGAG  
ATAGTGGGGGACCCCATGTTACTGAAGTGGGAAGGACCAGTTTCTTA  
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA  
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAAGGAAA  
AAACAAAGCTCACTTAATGAAAGATGGATTTC AAGGTTAATTTCATT  
GGAATTGAAAATTAACAG



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FIG. 56B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu  
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala  
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe  
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu  
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr  
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys  
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn  
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys  
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu  
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser  
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr  
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser  
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe  
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val  
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr  
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn  
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn  
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr  
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly  
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln  
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe  
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser  
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu  
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr  
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 57A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG  
 GTGTTTCTGCATGTTCTCCATTCGGCTCCTGATGTGCAGGATTGCCCCA  
 GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC  
 AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC  
 ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTACCTCAG  
 AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG  
 GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG  
 TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT  
 GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT  
 GTGAGATAAAACTCTCCTTTTCCCTTACCATACCCTTTGACACGCTTC  
 AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA  
 TCAGCAGTCTAGTTCTTTTCATTGGAATGAATACAGCATTAAAGCTTG  
 TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 57B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
 His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
 Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
 Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
 Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
 Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
 Lys Ser

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FIG. 57C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC  
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA  
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTGGTGTGCTG  
GCTACTGCTACACCAGGGATCTGGTGTATAAAGGACCCAGCCAGGCCC  
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT  
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC  
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG  
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA  
TGAAAGAATAA

FIG. 57D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys  
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe  
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val  
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val  
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr  
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 58A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC  
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT  
GCACCGCCGAGCTTCCCGGATGAGGGCCCCCGGTGTGGTCAACCGG  
CGCGCCCCAGGTTCGTGAGGGACCCCGCCAGGCGCGGAGATGGGG  
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTG  
CTCCCTCTGGGCCTCCCAGTCTTGGGCGCCCCACCACGCCTCATCTGT  
GACAGCCGAGTCTTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG  
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT  
ATCACTGTCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT  
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG  
CTGTCGGAAGCTGTCTTGGCGGGGCCAGGCCCTGTTGGTCAACTCTTC  
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTG  
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCCAGAAGG  
AAGCCATCTCCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA  
ATCACTGCTGACACTTTCCGCAAACCTCTCCGAGTCTACTCCAATTC  
CTCCGGGGAAGGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG  
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC  
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC  
GTGCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA  
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC  
AACTCTGAGATCTAAGGATGTACAGGGCCAACTTGAGGGCCCAGAG  
CAGGAAGCATTCAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG  
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC  
AGGACACGCTTTGGAGGCGATTACCTGTTTTGCACCTACCATCAGG  
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG  
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA  
CCGGGCTGGTGGGAACCATGAAGACAGGATGGGGCTGGCCCTCTGG  
CTCTCATGGGGTCCAAAGTTTGTGTATTCTTCAACCTCATTGACAAGA  
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 58B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser  
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser  
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr  
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val  
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu  
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser  
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile  
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe  
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr  
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

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FIG. 59A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT  
CTCTGCACCCGCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC  
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA  
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT  
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCGCTGGAGCTGT  
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG  
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA  
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA  
ACCTGAAGGACTTTCTGCTTGTCATCCCTTTGACTGCTGGGAGCCAG  
TCCAGGAGTGA

FIG. 59B

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro  
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu  
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr  
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg  
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro  
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu  
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 60A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG  
GGTTCCTCTGGCTGTTACTGCCAGGACCCATATGTAAAAAGAAGCAGA  
AAACCTTAAGAAAATATTTTAATGCAGGTCATTTCAGATGTAGCGGATA  
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT  
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCT  
TTTTAAAAAAGTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA  
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG  
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT  
GAATGTCCAACGCAAAGCAATACATGAACATCCAAAGTGATGGCTG  
AACTGTCGCCAGCAGCTAAAAACAGGGAAGCGAAAAAGGAGTCAGAT  
GCTGTTTCGAGGTCGAAGAGCATCCAGTAA

FIG. 60B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu  
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr  
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile  
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser  
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val  
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys  
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln  
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys  
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

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FIG. 61A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT  
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA  
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC  
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC  
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA  
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC  
CCTGGGGACCAAGGCTGACACTACGATGAAATCCTGGAGGGCCTGA  
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC  
CAGGAACCTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT  
GACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCTAGTGG  
ATAAGTTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC  
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG  
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG  
GAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTT  
AAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG  
AGGACTTCCACGTGGACCAAGGTGACCACCGTGAAGGTGCCTATGATG  
AAGCGTTTAGGCATGTTAACATCCAGCACTGTAAGAAAGCTGTCCAG  
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT  
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC  
CAGGATATCATCACCAAGTTCTTGAAAAATGAAGACAGAAGGTCTGC  
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA  
GAGCGTCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG  
CTGACCTCTCCGGGGTCAAGAGGAGGCACCCCTGAAGCTCTCCAAG  
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC  
TGCTGGGGCCATGTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA  
GGTCAAGTCAACAAACCTTTGTCTTCTTAATGATTGAACAAAATAC  
CAAGTCTCCCCCTTTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT  
AACTGCCTCTCGCTCCTCAACCCCTCCCTCCATCCCTGGCCCCCTCC  
CTGGATGACATTAAAGAAGGGTTGAGCTGG



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FIG. 61B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser  
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe  
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe  
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp  
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala  
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln  
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val  
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val  
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys  
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val  
Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val  
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser  
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro  
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys  
Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile  
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys  
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala  
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro  
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val  
Val Asn Pro Thr Gln Lys

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FIG. 62A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTT  
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT  
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA  
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC  
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGGGCATCAGGT  
GCCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT  
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT  
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG  
GATGGAGCTGAGTATGGGGCCCCATCCAGGCTAATCACACGGGCACAG  
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTCCAGAAAGTGAAG  
GGATTGGAGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC  
CTGTCACCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA  
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA  
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCGA  
GTTGCACAACCTCAGCCTCCAGAGGAAGATACCAAGCTCAAGATAC  
CCCTGATTACCGAGCCCTGCAGTTGGCCAGCGTCCCGTTTCACTCC  
TTGCCAGCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG  
GTGAATGGGAAGGGGTCACCTAAGGGACAGCCCGGAGACATCTACC  
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCCTATGCTG  
AGCACAAAGTTACAGTTCTGGGCAGTGACAGCTGAAATGAGCCTTCT  
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCT  
GAACATCAGCGAGACTTCATTGCCCCTGACCTAGTCCCTACCCCTCGCC  
AACAGTACTCACCACAAATGTCCGCCTACTCATGCTGGATGACCAACGC  
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC  
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTCT  
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA  
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTCTGGG  
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC  
CACAGCATCATCAGAACCTCCTGTACCATGTGTGTCGGCTGGACCGAC  
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA  
CTTTGTCGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTA  
CAAAACAGCCCATGTCTACCACCTTGGCCAGCTCAGCAAGTTCATTCC  
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC  
TGGACGCAGTGGCACTGATGCATCCCAGTGGCTCTGCTGTTGTGGTCTG  
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG  
CTGTGGGCTTCTTGAGACAATCTCACCTGGCTACTCCATTACACCT  
ACCTGTGGCATCGCCAGTGTGAGCAGATACTCAAGGAGGCATGG  
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAAGTCAACACGCTGTCTG  
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 62A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT  
 GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC  
 CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT  
 TGGAAACT

FIG. 62B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser  
 Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser  
 Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys  
 Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr  
 Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly  
 Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu  
 Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Lys Ser Tyr Phe Ser  
 Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser  
 Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser  
 Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu  
 Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile  
 Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu  
 His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp  
 Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg  
 Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val  
 Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro  
 Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser  
 Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn  
 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu  
 Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr  
 Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu  
 Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn  
 Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu  
 Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 63A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG  
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTTCAGAA  
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAAACGCA  
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA  
GCAACCGGGTGGAATATTGCTGGTGC AACAGTGGCAGGGCACAGTGC  
CACTCAGTGCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG  
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG  
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA  
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGACAGTGGAGCAC  
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG  
GCCCAGAAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG  
GCCTGGGGAACCACAACCTACTGCAGAAACCCAGATCGAGACTCAAA  
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT  
GCAGCACCCCTGCGCTCTCTGAGGGAAACAGTGACTGCTACTTTGGG  
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC  
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC  
AGCACAGAACCCAGTGCCCAGGCACTGGGCCTGGGCAACATAATT  
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG  
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCCTCTGCTC  
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG  
GAGGGCTCTTCGCGGACATCGCCTCCACCCCTGGCAGGCTGCCATCT  
TTGCCAAGCACAGGAGGTGCGCGGGAGAGCGGTTCTGTGCGGGGGC  
ATACTCATCAGTCTCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG  
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA  
CCGGTGGTCCCTGGCGAGGAGGAGCAGAAATTGAAAGTCGAAAAA  
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT  
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCCTGTGCCAGGAGA  
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGCGGACCTGCAGCTG  
CCGGA CTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC  
CTTGCTCTCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTGAGCT  
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG  
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC  
CAGGCAAACTTGACGACGCCTGCCAGGGCGATTCTGGGAGGCCCCCT  
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT  
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG  
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC  
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

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FIG. 63B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val  
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr  
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp  
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly  
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn  
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro  
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu  
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys  
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp  
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp  
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser  
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr  
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met  
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu  
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His  
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser  
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe  
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser  
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser  
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly  
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys  
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu  
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg  
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu  
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn  
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro  
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly  
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg  
Asp Asn Met

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FIG. 64A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA  
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATCTTGCACTTG  
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAAGAAAAACAAAGAAA  
ACACAGCTACAACCTGGAGCATTTACTGCTGGATTTACAGATGATTTTG  
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC  
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC  
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA  
GCTCAAAGCAAAAACTTTCACTTAAGACCCAGGGACTTAATCAGCAA  
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTC  
TGTGTGAATATGCAGATGAGACAGCAACCATGTAGAATTTCTGAAC  
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA  
TTAAGTGCTTCCCCTTAAACATATCAGGCCTTCTATTATTTATTTA  
AATATTTAAATTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG  
TAACTATTATCTTAATCTTAAACTATAAATATGGATCTTTATGAT  
TCTTTTGTAAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC  
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG  
ATTGGTTAGTAAACTATTTAATAAATTTGATAAATATAAAAAAAAAA  
AAACAAAAAAAAAAAA

FIG. 64B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn  
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu  
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn  
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr  
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val  
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser  
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu  
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys  
Gln Ser Ile Ile Ser Thr Leu Thr

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FIG. 65A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCT  
GCTTTAGTGGCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCA  
TGGGACTATATGCAAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG  
ATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT  
GTACAAAAAGACTCTGTTTGTAGAATTACGCGATCACCTTTTCAACAT  
CGCTAAGCCAAAGGCCACCCTGGATGGGTCTGCTAGGTCTACCATCC  
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT  
TCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT  
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG  
AAGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTGGCAG  
GTCCTGAAAGAGAAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC  
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG  
CCTCATTGGAGCCCTACTAGTATGTAGAGAAAGGAGTCTGGCCAAAGG  
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTGCTGTATTG  
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA  
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCATAAAATGCACACAG  
TCAATGGTTATGTAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA  
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGACCCACTCCTGAA  
GTGCACTCAATATTCTCGAAGGTCACACATTTCTTGTGAGGAACCAT  
CGCCAGGCGTCTTGGAAATCTCGCCAATAAATTTCTTACTGCTCAA  
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTGTCAATCTCTT  
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAAGTACAGACTGT  
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG  
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG  
ATGATGACAACTCTCCTTCTTTATCCAAATTCGCTCAGTTGCCAAGA  
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC  
TGGGACTATGCTCCCTTAGTCTCGCCCCGATGACAGAAAGTTATAAA  
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA  
AAAAGTCCGATTTATGGCATACACAGATGAAACCTTAAAGACTCGTG  
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG  
AAGTTGGAGACACACTGTTGATTATTTAAGAATCAAGCAAGCAGA  
CCATATAACATCTACCCCTACGGAATCACTGATGTCCGCTCTTTGTAT  
TCAAGGAGATTACCAAAAAGGTGTAACACATTTGAAGGATTTTCCAAT  
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGAAGTGTAGAAG  
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA  
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTTGGCCCT  
TCTCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACAGATA  
ATGTCAGACAAGAGGAATGTCATCCTGTTTCTGTATTTGATGAGAAC  
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTCTCCCAATCCA  
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCAACATCAT  
GCACAGCATCAATGGCTATGTTTTGTAGTTTGTGATTTGTCAGTTTG  
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA  
CTGACTTCCTTTCTGTCTTCTCTCTGGATATACCTTCAAACACAAAAAT

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FIG. 65A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAAAAGTGT  
CTTCATGTCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA  
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT  
AGTTGTGACAAGAACTGGTGATTATTACGAGGACAGTTATGAAGA  
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA  
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCAAAAGCAATTT  
AATGCCACCACAATTCCAGAAAAATGACATAGAGAAGACTGACCCTTG  
GTTTGCACACAGAACACCTATGCCCTAAAATACAAAATGTCTCCTCTA  
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT  
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC  
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA  
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCC  
TGAGTCAGGCCTCCAATTAAAGATTAAATGAGAACTGGGGACAACTG  
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA  
AATAATCTGATTTCAACAATTCCATCAGACAAATTGGCAGCAGGTACT  
GATAATACAAAGTTCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT  
AGTCAATTAGATACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT  
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATCAAA  
GTTGTTAGAATCAAGTTTAATGAATAGCCAAGAAAGTTTCATGGGGAA  
AAAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAAGA  
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT  
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT  
AATAGAAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG  
TCCATCAGTCTGGCAAAATATATTAGAAAAGTGACACTGAGTTTAAAA  
AAGTGACACCTTTGATTTCATGACAGAAATGCTTATGGACAAAAATGCT  
ACAGCTTTGAGGCTAAATCATATGTCAAATAAAACTACTTCATCAAA  
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA  
GATGCACAAAATCCAGATATGTGCTTCTTTAAGATGCTATTCTTGCCA  
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA  
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCTTAGGACCCAG  
AAAAATCTGTGGAGGTCAGAAATTTCTGTCTGAGAAAAACAAAGTG  
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA  
TGGTTTTTCCAAGCAGCAGAAAACCTATTCTTACTAACTTGGATAATT  
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA  
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTGCCTC  
AGATACATACAGTGAAGTGGCACTAAGAATTTCAATGAAGAACCTTTTC  
TTACTGAGCACTAGGCAAAAATGTAGAAGGTTTCATATGACGGGGCATA  
TGCTCCAGTACTTCAAGATTTTAGGTCATTAATGATTCAACAAATAG  
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA  
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAAATGTAGAGAAATAT  
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAATTTTG  
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA



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FIG. 65A-3

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC  
CCAGTGGTCCAAAAACATGAAACATTTGACCCCAGACCCCTCACAC  
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC  
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAAATAGA  
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA  
TATATCTGACCAGGGTCTTATTCGAAGACAACCTCTTCTCATCTTCCAG  
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT  
TTCTTACAAGGAGCCAAAAAATAACCTTCTTTAGCCATTCTAACC  
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG  
TGCCACAAATTGAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC  
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA  
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAACTAGCAATG  
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA  
CAGAGGGAGCGATTAAAGTGAATGAAGCAAAACAGACCTGAAAAAGT  
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAGACTCCCTCCAA  
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC  
AAAAGAAGAGTGGAAATCCCAAGAGAAGTCACCAGAAAAAACAGCT  
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT  
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG  
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA  
AACCCACCAAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC  
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT  
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAAATC  
AGAGCCCCCGACGCTTTCAAAAGAAAAACAGACACTATTTTATTGCTG  
CAGTGGAGAGGCTTGTGGGATTATGGGATGAGTACGCTCCCAACATGTT  
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT  
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT  
GGAGAACTAAATGAACATTGGGACTCCTGGGGCCATATATAAGAGC  
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC  
GTCCTATTCTCTTATCTAGCCTTATTTCTTATGAGGAAGATCAGAG  
GCAAGGAGCAGAACCTAGAAAAAACTTTGTCAAGCCTAATGAAACCA  
AAACTTACTTTTGAAAAGTGCAACATCATATGGCACCCACTAAAGAT  
GAGTTTGAAGTCAAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA  
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT  
AACACACTGAACCTGCTCATGGGAGACAAGTGACAGTACAGGAATT  
TGCTCTGTTTTTACCACATCTTTGATGAGACCAAAAGCTGGTACTTCACT  
GAAAATATGGAAAGAAACTGCAGGGCTCCCTGCAATATCCAGATGGA  
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA  
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAAGGA  
TTCTGATGGTATCTGCTCAGCATGGGCAGCAATGAAAAACATCCATTCT  
ATTCATTTCAAGTGACATGTGTTCACTGTACGAAAAAAGAGGAGTA  
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGAA

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FIG. 65A-4

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGAATGCCTTATTGG  
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA  
TAAGTGTACAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT  
TCAGATTACAGCTTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG  
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAGGAG  
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC  
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT  
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA  
CTTATCGAGGAAATTCCTACTGGAACCTTAATGGTCTTCTTGGCAATG  
TGGATTTCATCTGGGATAAAAACACAATATTTTAAACCCCTCAATTATTG  
CTCGATACATCCGTTTGCACCCACTCATTATAGCATTTCGCAGCACTC  
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT  
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA  
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA  
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA  
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA  
CAGGAGTAACCTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT  
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC  
TCTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA  
CTCCTTCACACCTGTGGTGAACCTCTAGACCCACCGTTACTGACTCG  
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAAGATTGCCGTGAG  
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC  
CACTGCAGCACTGCCACTGCGCGTCACCTCTCCCTCCTCAGCTCCAGG  
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC  
AGACACTGCCTTGAAGCCTCCTGAATTAACATATCATCAGTCTGCATT  
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACCTTA  
CCTATTTTCTGCAGCTGCTCCAGATTACTCCTTCCTTCCAATATAACT  
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCAATCTTCCCTG  
AAAAGTTAGCCCTCTCAGAGTCACCACCTTCTCTGTTGTAGAAAACT  
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTCAAGT  
TAAGCCTCATACGTTTAAAAATAAACTCTCAGTTGTTTATTATCCTGA  
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT  
GGAGTCAAAAGGCAAATCATTGGACAATCTGCAAAATGGAGAGAA  
TACAATAACTACTACAGTAAAGTCTGTTCTGCTTCTTACACATAGA  
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA  
AACTAGCATTTCTTAACTGAGAATTATAGATGGGGTTCAAGAATCCC  
TAAGTCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC  
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT  
GACCAATAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG  
AAATAAAATAACAATGTCTTCTGAAATTTGTGATGGCCAAGAAAGA  
AAATGATGA

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## FIG. 65B-1

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser  
 Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser  
 Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe  
 Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His  
 Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile  
 Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro  
 Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr  
 Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly  
 Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro  
 Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn  
 Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys  
 Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser  
 Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg  
 Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu  
 Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro  
 Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln  
 Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp  
 Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu  
 Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn  
 Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val  
 Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys  
 Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr  
 Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr  
 Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro  
 Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser  
 Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg  
 Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile  
 Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg  
 Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser  
 Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn  
 Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg  
 Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln  
 Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val  
 Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu  
 Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys  
 His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val  
 Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe  
 Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr  
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn  
 Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln  
 Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp

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## FIG. 65B-2

Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu  
 Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu  
 Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn  
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val  
 Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr  
 Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu  
 Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu  
 Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly  
 Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn  
 Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly  
 Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly  
 Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu  
 Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp  
 Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser  
 Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp  
 Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser  
 Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala  
 Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg  
 Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro  
 Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu  
 Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly  
 Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp  
 Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile  
 Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr  
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln  
 Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg  
 Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys  
 Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val  
 Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe  
 Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu  
 Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn  
 Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu  
 Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile  
 Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile  
 Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro  
 Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu  
 Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr  
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr  
 Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser  
 Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro  
 Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu

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## FIG. 65B-3

Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys  
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu  
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu  
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile  
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly  
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg  
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg  
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu  
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg  
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp  
 Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val  
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro  
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg  
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro  
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu  
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val  
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr  
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu  
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln  
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu  
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr  
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro  
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly  
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys  
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr  
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu  
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr  
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln  
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala  
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile  
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly  
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile  
 Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr  
 His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn  
 Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr  
 Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu  
 His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu  
 Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln  
 Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser  
 Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe  
 Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu  
 Leu Thr Arg Tyr Leu Arg Ile His

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FIG.65B-4

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu  
Ala Gln Asp Leu Tyr

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FIG. 66A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC  
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG  
GCGCGCCTGCTTCTCTGCGTCCTGGTCTGTGAGCGACTCCAAAGGCAGC  
AATGAACTTCATCAAGTTCATCGAACTGTGACTGTCTAAATGGAGGA  
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCAGTGGTGCAACTGC  
CCAAAGAAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAC  
CTGCTATGAGGGGAATGGTCACTTTACCGAGGAAAGGCCAGCACTG  
ACACCATGGGCCGGCCCTGCCCTGGAACCTGCGCACTGTCCTTC  
AGCAAACGTACCATGCCACAGATCTGATGCTCTTCAGCTGGGCTGG  
GGAAACATAATTACTGCAAGAACCCAGACAACCGGAGGCGACCCCTGG  
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCGAAGAGTGCATGGT  
GCATGACTGCGCAGATGGAAAAAGCCCTCCTCTCCTCCAGAAGAAT  
TAAATTTTCAGTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA  
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTTCGGCC  
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG  
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT  
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA  
GGCTTAACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAAC  
CTCATCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC  
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA  
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA  
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA  
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA  
AGCTGATTTCACCGGGAGTGTGAGCAGCCCCACTACTACGGCTCTG  
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGGA AAAA  
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA  
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC  
CCTGAAGGACAAGCCAGGCGTCTACAGAGAGTCTCACACTTCTTAC  
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA  
GGGTCCCCAGGGAGGAAACGGGCACCCCGCTTCTGTCTGGTTGTG  
ATTTTTCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA  
AGAT

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FIG. 66B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser  
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly  
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys  
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn  
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro  
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg  
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His  
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys  
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr  
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys  
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu  
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys  
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg  
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro  
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr  
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp  
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val  
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser  
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu



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FIG. 67A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA  
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAAATTGTCATCA  
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC  
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG  
GCACTGGCGGCCCTACTGCAGGGGGCCGTGTCCCTGAAGATCGCAGC  
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT  
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT  
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG  
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT  
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCTGTGTA  
CAGGCCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG  
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT  
GTCAGGTTCTTCTCCCGTTTACAGAGGTCAGGGAGTTTGCCATTGTT  
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT  
CTATGACGTCTACCTGGATGTCCAAGAGAAAATGGGGCTTGGAGGACG  
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT  
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGCG  
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT  
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGGCGCCGTTGTT  
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG  
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG  
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAAGTGCAG

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FIG. 67B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu Leu Gln  
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile  
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu  
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro  
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln  
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp  
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln  
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser  
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln  
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
Glu Val Met Leu Lys

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FIG. 68A

GCTGCATCAGAAGAGGGCCATCAAGCACATCACTGTCCTTCTGCCATGG  
CCCTGTGGATGCGCCTCCTGCCCCCTGCTGGCGCTGCTGGCCCTCTGGG  
GACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGCGGCTCAC  
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT  
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA  
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG  
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT  
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG  
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA  
TGAATAAAGCCCTTGAACCAGC

FIG. 68B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly  
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val  
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr  
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro  
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile  
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 69A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT  
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCTT  
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA  
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC  
GGGCCAGGGTTACCCCCACCACACGGCGGTCTTTTGGGGTGGAGCCC  
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG  
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC  
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAACCTCCACAACA  
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCTATATTTTCCT  
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCTGTTCCGACTACTGTC  
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCTGCACCGAAC  
ATGGAGAGCACAACATCAGGATTCTAGGACCCCTGCTCGTGTACA  
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCAATACACAGAGTCT  
AGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGGAGCACCCACGTG  
TCCTGGCCAAAATTTCGAGTCCCCAACCTCCAATCACTCACCACCTC  
TTGTCTCCAATTTGTCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT  
ATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC  
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA  
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT  
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC  
GGAAACTGCACTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA  
TTCTATGGGAGTGGGCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA  
GTGCCATTTGTTTCACTGGTTTCGACGGGCTTTCCCCACTGTTTGGCTTT  
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT  
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC  
ATTGA

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FIG. 69B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro  
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn  
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile  
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu  
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro  
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg  
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu  
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val  
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp  
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu  
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser  
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr  
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu  
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu  
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala  
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp  
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala  
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro  
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu  
Trp Val Tyr Ile

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FIG. 70A

CGAACCACCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA  
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC  
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGC  
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT  
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG  
AAGTATTTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG  
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA  
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA  
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG  
CGCCTCTGACAGCAACGCTCTATGACCTCCTAAAGGACCTAGAGGAAG  
GCATCCAAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT  
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA  
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG  
GAAGGACATGGCAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCG  
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG  
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT  
GCCACCAGCCTTGCTTAATAAAATTAAGTTGCATC

FIG. 70B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu  
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp  
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 71A

ATGGCGCCCGTCGCCGCTCTGGGCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCTTGCCCCGCCAGGTGGCATTTACACCCTA  
CGCCCCGGAGCCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC  
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA  
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG  
GACAGCACATACACCAGCTCTGGAACCTGGGTTCCCGAGTGCTTGAG  
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAAACTCAAGCCTGCAC  
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG  
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGTGCGCAAG  
TGCCGCCCGGGCTTCGGCGTGGCCAGACCAGGAACCTGAAACATCAGA  
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC  
ATCCACGGATATTTGCAGGCCCCACAGATCTGTAACGTGGTGGCCAT  
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA  
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC  
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGTCC  
AAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG  
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC  
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAACCTGTGTATCATGAC  
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC  
CTCACTTGCTGCGGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG  
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA  
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAGC  
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC  
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG  
TCAATGTCACTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT  
CACAGTGCTCTCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC  
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGTCCCCCTTCTCCAAGGA  
GGAATGTGCTTTTCGCTCACAGCTGGAGACGCCAGAGACCCTGTGG  
GGAGCACCGAAGAGAAGCCCCCTGCCCCCTTGGAGTGCCTGATGCTGG  
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTGAGCCAAGG  
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGGCCCTGGTCTT  
CCAGG

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## FIG. 71B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala  
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser  
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys  
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys  
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln  
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val  
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr  
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val  
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr  
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln  
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly  
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val  
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro  
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg  
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly  
Glu Ala Arg Ala Ser Thr Gly Ser Ser Ser Asp Ser Pro Gly Gly His Gly Thr Gln  
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Ser Asp His Ser Ser Gln Cys  
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro  
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu  
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro  
Asp Ala Gly Met Lys Pro Ser



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FIG. 72A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro  
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 72B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg  
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr  
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys  
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
Gly Thr Leu Val Thr Val Ser Ser

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## FIG. 73A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr  
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp  
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp  
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser  
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr  
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ser

## FIG. 73B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys  
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser  
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe  
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 74A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA  
 GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC  
 ATCCACTGGTATCAGCAAAAGAACAATGGTTCTCCAAGGCTTCTCATA  
 AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC  
 AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT  
 GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC  
 ACGTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA  
 GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT  
 CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG  
 TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA  
 TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG  
 AGGTTCAACATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA  
 ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG  
 AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC  
 ACAGTCTCC

FIG. 74B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val  
 Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln  
 Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly  
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn  
 Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro  
 Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser  
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly  
 Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu  
 Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu  
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr  
 Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg  
 Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 75A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGGTTCCA  
GGTTCCACTGGTGACGTACGGCGAGGGCCCCGGAGCCTGCGGGGCAG  
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC  
TGCTGGTCCGCCACTGCGTGCCCTGCGGGCTCCTGCGCACGCCGCGGC  
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG  
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTTCGACA  
AAACTCACACATGCCCACCGTGCCACGACCTGAACTCCTGGGGGGA  
CCGTCAGTCTTCCTCTTCCCCC AAAACCCAAGGACACCCTCATGATC  
TCCCGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGA  
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC  
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA  
CCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTGAATGG  
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA  
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG  
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT  
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT  
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC TACAAGACCAG  
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC  
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC  
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT  
CCCTGTCTCCCGGGAAATGA

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FIG. 75B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser  
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala  
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala  
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro  
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 76

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro  
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 77

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys  
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe  
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr  
Leu Val Thr Val Ser Ala

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FIG. 78

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys



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FIG. 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
Thr Leu Val Thr Val Ser Ser

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FIG. 80

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro  
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
Ser Phe Asn Arg Gly Glu Cys

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FIG. 81

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His  
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 82A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA  
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC  
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG  
CTCAAGTGTAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTC  
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC  
TGTTGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTACAAT  
CAGCAGAGTGGAGGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT  
GGACTAGTAACCCACCCACGTTTCGGAGGGGGGACCAAGCTGGAATC  
AAA

FIG. 82B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser  
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu  
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Val Ser Tyr Ile His Trp Phe Gln  
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser  
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn  
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 83A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG  
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG  
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT  
ACCAGTTACAATATGCACTGGGTAACACAGACACCTGGTCGGGGCCCT  
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA  
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA  
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG  
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC  
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 83B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys  
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys  
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp  
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ala

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FIG. 84A

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCATTTG  
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG  
AGCTGGGTACGTCTCCATTCAGTGATCAGCAGTAACACAGACCC  
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCTTGTCGCTGTTGCTA  
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCT  
CCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTC  
AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC  
CCTGACCAGCGGGGTGCACACCTTCCCGGTGTCTTACAGTCTCAGG  
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA  
AGGTGGACAAGAAAAGCAGAGCCCAAATCTTGTGACAAAACCTACACA  
TGCCCAACCGTGGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC  
CTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCT  
GAGGTCAATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA  
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC  
GTCCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGACTACAA  
GTGCAAGGTCTCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCA  
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTG  
CCCCATCCCGGGATGAGCTGACCAGGAACCAGGTACGCTGACCTG  
CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA  
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGTG  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGACAAG  
GACAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG  
TAAATGAGGATCCGTTAAACGTTACCAACTACCTAGACTGGATTCGT  
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCT  
TCTAGTTGCCAGCCATCTGTTGTTGCCCCCTCCCCGTCTTCTTGA  
CCCTGGAAGGTGCCACTCCCACTGTCTTTTCTAATAAAATGAGGAAA  
TTGCATCGCATTGTCTGAGTAGGTGTCTATTCTATTCGGGGGTGGGG  
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA  
TGCTGGGGATGCGGTGGGCTCTATGGAACAGCTGGGGCTCGACAGC  
GCTGGATCTCCCGATCCCCAGCTTGTCTTCTCAATTTCTTATTGCTA  
ATGAGAAAAAAGGAAAAATTAATTTTAAACCAATTCAGTAGTTGAT  
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCAGCATTCTAGGGAGAAATATGCTT  
GTATCAACCGAAGCCTGATTCGGTAGAGCCACACCTTGGTAAAGGCC  
ATACTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 84B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG  
ACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAG  
AGCTGGGTACGTCCTCACATTACGTGATCAGCACTGAACACAGACCC  
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCCTTGTCGCTGTTGCTA  
CGCGTGTCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT  
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC  
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAATCAGGGCGC  
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGG  
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCA  
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA  
TGCCACCCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC  
CTCTTCCCCCCTAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCT  
GAGGTCAACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGT  
CAAGTTCACCTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA  
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC  
GTCTTACCCGTCTTGCACCAGGACTGGCTGAATGGCAAGGACTACAA  
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  
TCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTG  
CCCCATCCCCGGGATGAGCTGACCAGGAACCAGGTGACCGTGCACCTG  
CCTGGTCAAAAGCCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA  
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG  
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG  
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGTATGGATTCCGTG  
ACAACATGCGCGCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT  
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCCTCCTTGA  
CCCTGGAAGGTGCCACTCCCAGTGTCTTTCCTAATAAAATGAGGAAA  
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG  
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA  
TGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGACAGC  
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA  
ATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTTCAGTAGTTGAT  
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCTACCGCAAGCCTGATTCCGTAGAGCCACACCTTGGTAAAGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 84C

GCTGCGATTTCGCGCCAAAACCTTGACGGCAATCCTAGCGTGAAGGCTG  
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT  
CGTCGCCGTGTCCCAAAATATGGGGATTGGCAAGAACGGAGACCTAC  
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC  
ACAACCTCTTCAGTGGAAGGTAAACAGAAATCTGGTGATTATGGGTAG  
GAAAACCTGGTTCTCCATTCTGAGAACAAATCGACCTTTAAAGGACA  
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA  
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA  
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG  
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT  
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACAGCTTTTCCC  
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG  
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA  
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAGTTCTCTGC  
TCCCCTCCTAAAGTCAATGCATTTTATAAGACCATGGGACTTTTGCTG  
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT  
TTGCCCTCCCCCGTGCCTTCCCTTGACCTGGAAGGTGCCACTCCCAC  
TGTCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG  
GTGTCACTTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG  
AGGATTGGGAAGACATAAGCAGGCATGTCTGGGGATGCGGTGGGCTCT  
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTCTT  
ATTTGCATAATGAGAAAAAAGGAAAAATTAATTTAACACCAATTCA  
GTAGTTGATTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA  
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC  
AGAGCTGAGACTCTAAGCCAGTGAGTGGCAGCAGCATTCTAGGGAGA  
AATATGCTTGTATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG  
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGGCAGGAGCCAGGG  
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTC  
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAAACA  
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT  
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT  
GTTCCGGCTGTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGA  
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT  
CGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG  
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG  
CAGGATCTCCTGTCTCTCACCTTGCTCCTGCCAGAAAGTATCCATC  
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC  
CCATTGACACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCG  
GATGGAAGCCGCTTGTGTCGATCAGGATGATCTGGACGAAGAGCATC  
AGGGGCTCGCGCCAGCCGAACCTGTTGCCAGGCTCAAGGCGCGCATG  
CCCCACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTCCG



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FIG. 84D

AATATCATGGTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC  
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG  
TGATATTGCTGAAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGT  
GCTTTACGGTATCGCCGCTTCCCGATTTCGACGCGCATCGCCTTCTATC  
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC  
CGACCAAGCGACGCCAACCTGCCATCAGGAGATTTCGATTCCACCG  
CCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTCCGGGACGCCG  
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC  
ACCCCAACTTGTTTATTGACGCTTATAATGGTTACAAATAAAGCAATA  
GCATCACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTT  
GTGGTTTGTCCAAATCATCAATCTATCTTATCATGTCTGGATCGCGG  
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC  
TGTTGTAATTTGTTATCCGCTCACAATCCACACAACATACGAGCCGG  
AGCATAAAGTGTAAGGCTGGGGTGCCTAATGAGTGAGCTAACTCAC  
ATTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTC  
GTGCCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGCGGTT  
TGCGTATTGGGCGCTCTCCGCTTCCGCTCACTGACTCGCTGCGCTC  
GGTCGTTGCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA  
TACGTTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA  
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC  
TGCGCTTTTCCATAGGCTCCGCCCTGACGAGCATCACAATAATC  
GACGCTCAAGTCAGAGGTGGCGAAAACCGACAGGACTATAAAGATAC  
CAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC  
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG  
GCGCTTTCTCAATGCTACGCTGTAGGTATCTCAGTTCCGTTAGGTC  
GTTCTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGAC  
CGCTGCGCTTATCCGGTAATCTCGTCTTGAGTCCAACCCGGTAAGA  
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG  
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTA  
ACTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTTGCTGA  
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA  
CAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATT  
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC  
GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG  
TCATGAGATTATCAAAAAAGGATCTTACCTAGATGCTTTTAAATTA  
AATGAAGTTTAAATCAATCTAAAGTATATAGCTAAACCTGGTCTG  
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC  
TATTTCTGTTTATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC  
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC  
GAGACCAACGCTCACCAGCTCCAGATTTATCAGCAATAAACCAAGCCA  
GCCGGAAGGGCCGAGCGCAGAGTGGTCCGCAACTTTATCCGCTC  
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAAGTAGTTCG

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FIG. 84E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG  
TGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC  
GATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTT  
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAAGTAAGTTGGCCGCGAGTG  
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCAATGC  
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT  
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA  
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC  
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG  
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAGTATCTTCA  
GCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGG  
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA  
TACTCATACTCTTCCTTTTCAATATTATTGAAGCATTTATCAGGGTTA  
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA  
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

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FIG. 85A

GACGTCGCGGCCGCTCTAGGCCCTCCAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCCTCGGCCCTCTGCATAAAATAAA  
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAAGTGGGGCG  
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA  
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT  
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCC  
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCACT  
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCTTATTGAG  
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT  
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA  
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC  
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCATTGACGTCAATG  
GGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA  
ACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGG  
GAGAGCCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT  
CAGCTTCTTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT  
TGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA  
GGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACT  
GGTTCAGCAGAAGCCAGGATCCTCCCCCAAACCCCTGGATTTATGCCA  
CATCCAACCTGGCTTCTGGAGTCCCTGTTCTCAGTGGCAGTGGGT  
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG  
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTG  
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT  
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCC  
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAG  
TGTCACAGAGCAGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA  
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC  
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT  
CAACAGGGGAGAGTGTTGAATTCAGATCCGTTAACGGTTACCAACTA  
CCTAGACTGGATTTCGTGACAACATGCGGCCGTGATATCTACGTATGAT  
CAGCCTCGACTGTGCCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC  
CCCCGTGCCCTTCCTTGACCCCTGGAAGGTGCCACTCCCACTGTCCTTCC

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FIG. 85B

TATAAAAATGAGGAAATTGCATCGCATTGCTGAGTAGGTGTCATTCT  
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG  
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA  
GCTGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTC AATG  
ACGGTAAATGGCCCCGCCTGGCATTATGCCAGTACATGACCTTATGGG  
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT  
GGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGATAGCGGTTTG  
ACTCACGGGGATTTC AAGTCTCCACCCCATGACGTC AATGGGAGTT  
TGTTTTGGCACCAAAATCAACGGGACTTCCAAAATGTCGTAACAACCT  
CCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC  
TATATAAGCAGAGCTGGGTACGTCTC AATTGAGTATCAGTGATCAGCACTGA  
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT  
CGCTGTTGCTACGCGTGTCTGTCCAGGTACAACCTGCAGCAGCCTGG  
GGCTGAGCTGGTG AAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG  
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAAACAGA  
CACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTATCCCGGAAAT  
GGTGATACTTCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC  
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA  
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG  
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGACCACGGTCACC  
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCACCC  
TCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT  
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACTCAGGCG  
CCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCTCAG  
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCACTTGG  
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGACCAACCC  
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTTGTGACAAAACCTCACAC  
ATGCCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT  
CCTCTTCCCCC A A A A C C C A A A G G A C A C C C T C A T G A T C T C C C G A C C C  
TGAGGTCACATGCGTGGTGGTGACGTGAGCCACGAAGACCTTGAGG  
TCAAGTTCAACTGTACGTGGAGCGGCTGGAGGTGCATAATGCCAAG  
ACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG  
CGTCTCACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGAGTACA  
AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACC  
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGATACACCT  
GCCCTCATCCCGGGATGAGCTGACCAAGAACCAGCAGCTGACACCT  
GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAG  
AGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT  
GGACTCCGACGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAA  
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG  
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTTCCCTGTCTCCGG  
GTAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT

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FIG. 85C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC  
TTCTAGTTGCGAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG  
ACCCCTGGAAGGTGCCACTCCCAGTGCCTTCTCAATAAAAATGAGGAA  
ATTGCATCGCATTGCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG  
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC  
ATGCTGGGGATGCGGTGGGCTCTATGGAACAGCTGGGGCTCGACAG  
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTCAT  
AATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGA  
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCATCACCCGAAGCCTGATTCCGTAGAGCCACACCTTGTAAGGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGCCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGATAGCTTGACAGCTCAGGGCTGCGATTTCG  
CGCCAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC  
CCCCGTGCCATCATGGTTCGACCATTTGAACGATCGTCGCCGTGTCC  
CAAAATATGGGATTGGCAAGAACGGAGACCTACCCCTGGCCTCCGCT  
CAGGAACGAGTTCAAGTACTTCAAAGAATGACCACAACCTCTTCAG  
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAAACCTGGTTC  
TCCATTCTTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT  
CTCAGTAGAGAACTCAAAGAACCACACGAGGACTCATTTTCTTTCG  
CAAAAGTTTGGATGATGCCCTTAAGACTTATTGAACAACCGGAATTGG  
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC  
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG  
ATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCAGAAATTGATTG  
GGGAAATATAAACTTCTCCAGAATACCCAGCGCTCCTCTGAT  
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA  
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCTCCTAA  
AGCTATGCATTTTATAAGACCATGGGACTTTTGTGCTTTAGATCA  
GCCTCGACTGTGCCCTTCTAGTTGCCAGCCATCTGTTGTTGCCCCCTCC  
CCGTGCCCTTCTTGACCCCTGGAAGGTGCCACTCCCATTGCTCTTCTTA  
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT  
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA  
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC  
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTATTTCATTAATG  
AGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA  
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCTGCA  
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGAG  
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC  
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGTAAGGGCCAAT  
CTGCTCACACAGGATAGAGAGGGGCAGGAGCCAGGGCAGAGCATATA  
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

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FIG. 85D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA,  
CGCAGGTTTCCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG  
GGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTC  
AGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC  
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA  
CGACGGGCGTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGG  
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG  
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA  
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC  
CAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG  
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC  
CAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG  
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG  
GAAAATGGCCGCTTTTCTGGATTTCAGCTGTGGCCGGCTGGGTGTG  
GCGGACCGCTATCAGGACATAGCGTTGGCTAGCCGTTCTCTCGTGTTCACGGTAT  
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTCGTGTTCACGGTAT  
CGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGA  
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC  
GCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGA  
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT  
CCAGCGCGGGGATCTCATGTGAGTTCTTCGCCACCCCACTTTGTT  
TATTGCAGCTTATAAATGGTTACAAATAAAGCAATAGCATCACAAATTT  
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA  
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCCTC  
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTG  
TATCCGCTCACAAATTCACACAACATACGAGCCGGAAGCATAAAGTG  
TAAAGCTTGGGTGCCTAATGAGTGAGCTAACTACATTAATTCGGTT  
TCGCTACTGCCCCGCTTTCCAGTCGGGAAACCTGTCTGTCGACGCTGCA  
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTATTGGGC  
GCTCTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCT  
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA  
CAGAATCAGGGGATAACGCAGGAAAGAATGTGAGCAAAAAGGCCA  
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTC  
ATAGGCTCCGCCCCCTTACGAGCATCACAAAAATCGACGCTCAAGT  
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC  
CCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTAC  
CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA  
ATGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAA  
GCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTT  
ATCCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

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FIG. 53A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA  
AGAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA  
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAAACATTAACCTTAT  
ACTTTTAAATTTAATGTATAGAAATAGAGATATACATAGGATATGTAAA  
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC  
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC  
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA  
AAGAGTGTATAAAGAAAAGCAAAAAGAGAAAGTAGAAAAGTAACACAGG  
GGCATTGGAAAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC  
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC  
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA  
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT  
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG  
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAAATCTCTCTTTCTCC  
TGCTTGAAGGACAGACATGACTTTGGATTTCCCGAGGAGGAGTTTG  
CAACCAGTTCACAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA  
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT  
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG  
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA  
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT  
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT  
GCCTGGGAGGTTGTGCAAGCAAGAAATCATGAGATCTTTTCTTTGTCA  
ACAAACTTGCAAGAAAGTTTAAAGAAGTAAGGAATGAAAACCTGGTTCA  
ACATGGAAATGATTTTCATTGATTTCGTATGCCAGCTCACCTTTTTATG  
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT  
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTAG  
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATTGCTGACTGATCCATT  
ATCTATTTAAATATTTTTAAATATTATTTATTTAACTATTTATAAAAC  
AACTTATTTTTGTTCTATATTATGTCATGTGCACCTTTGCACAGTGGTTA  
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGT  
CATTGAACTTTTGCTATGGAACCTTTGTACTTGTATTCTTTAAAAATG  
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA  
CTTCATTTGTCCATCAATATTATTTCAAGATATAAGATAAAAAATAAAC  
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC  
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA  
AAACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT  
ATGAAGAGAAGAAGGAACG

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FIG. 85E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG  
TAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCCTAACTACGGCTAC  
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC  
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC  
TGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAA  
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC  
TCAGTGGAACGAAAACTCACGTAAAGGGATTTTGGTCATGAGATTATC  
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAA  
ATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATG  
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC  
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG  
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC  
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG  
AGCGCAGAAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTA  
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTGCCAGTTAATAGTTTGC  
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGT  
TTGGTATGGCTTCATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTA  
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC  
CGATCGTTGTCAGAAGTAAGTTGGCCGCGAGTGTTATCACTCATGGTTA  
TGGCAGCACTGCATAATTCTCTTACTGTTCATGCCATCCGTAAGATGCT  
TTTCTGTGACTGGTGAGTACTCAACCAAGTCAATTCTGAGAATAGTGTA  
TGCGGCGACCCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAAATACC  
GCGCCAGATAGCAGAACTTTAAAAAGTGCTCATCATTGGAAAAACGTTCT  
TCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCCG  
ATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCA  
CCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAA  
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT  
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG  
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCCG  
GCACATTTCCCGAAAAAGTGCCACCT



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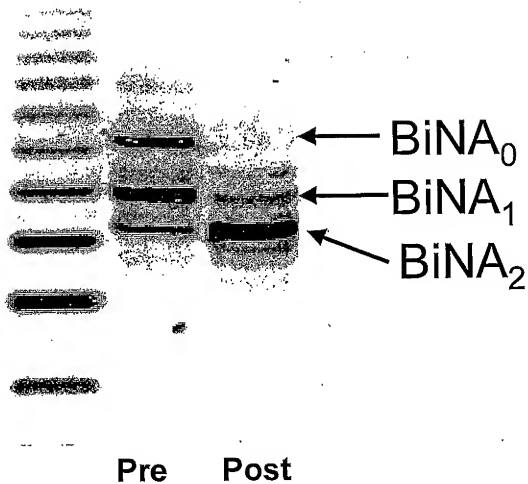


FIG. 86

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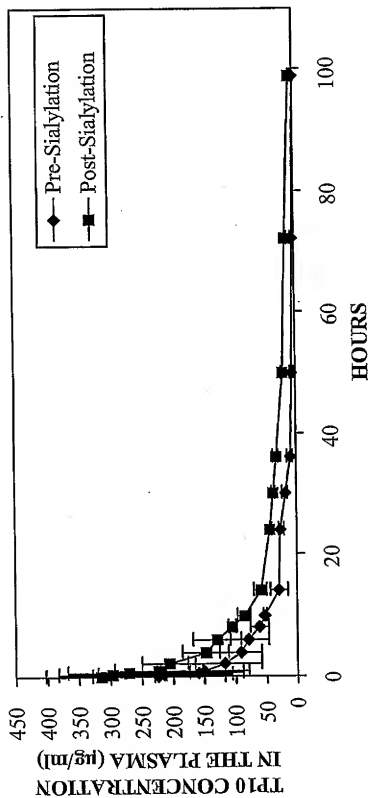


FIG. 87

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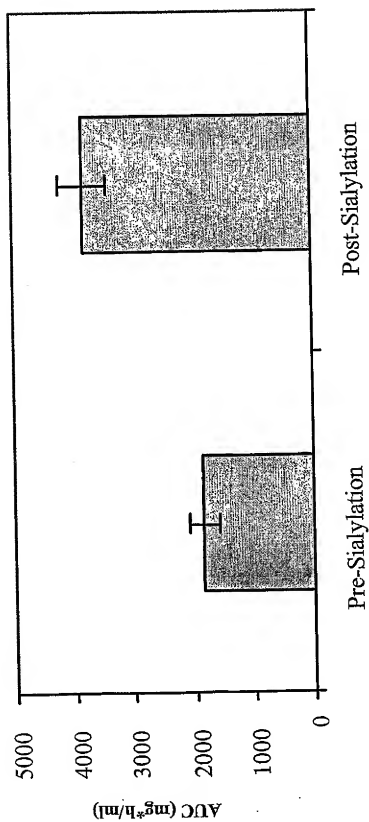


FIG. 88

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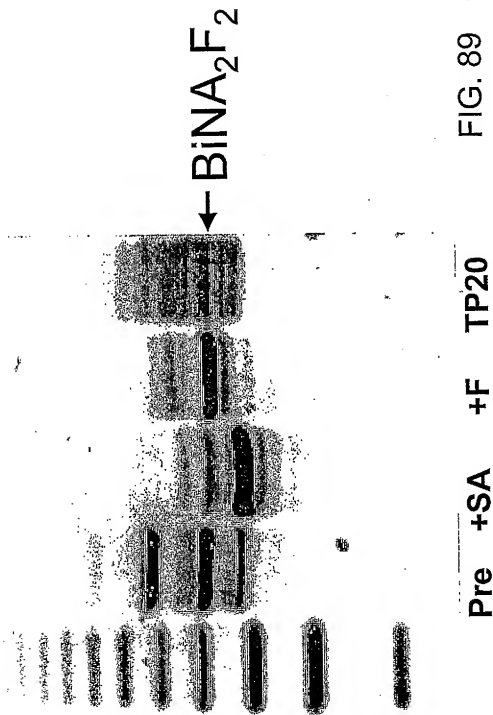


FIG. 89

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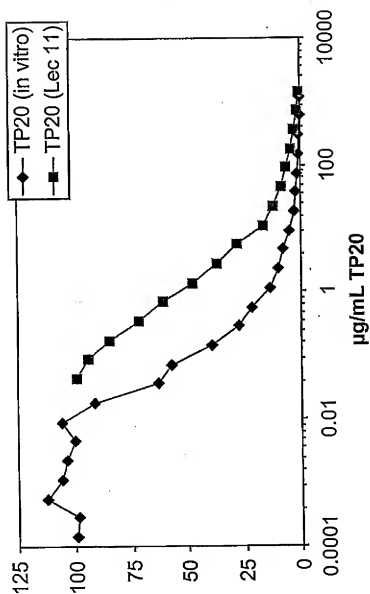


FIG. 90

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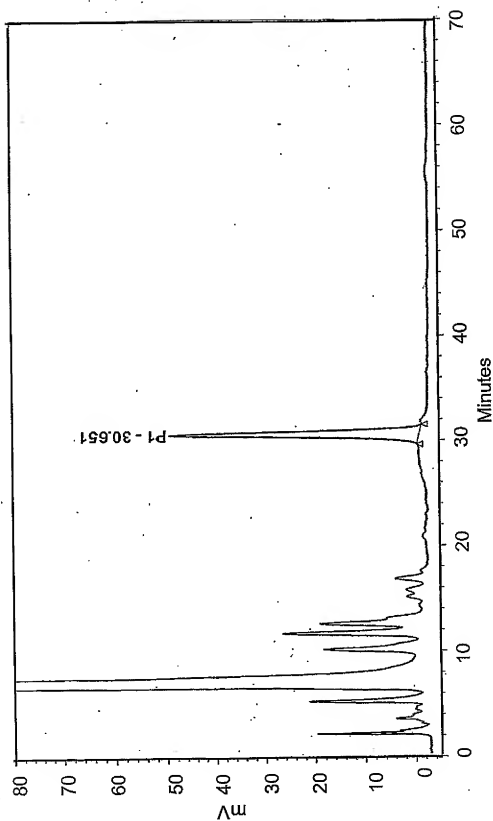


FIG. 91

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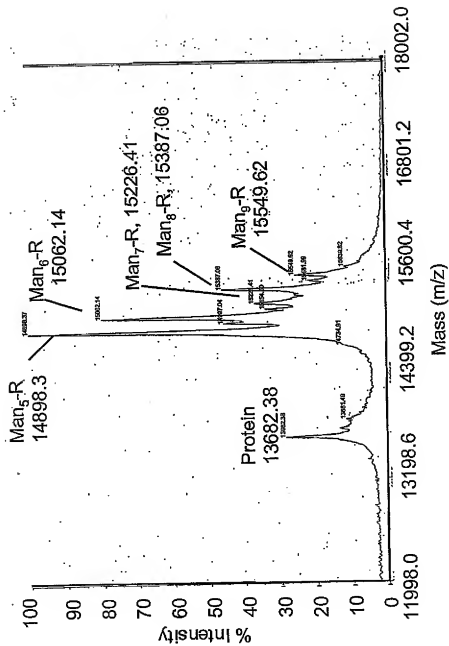


FIG. 92A

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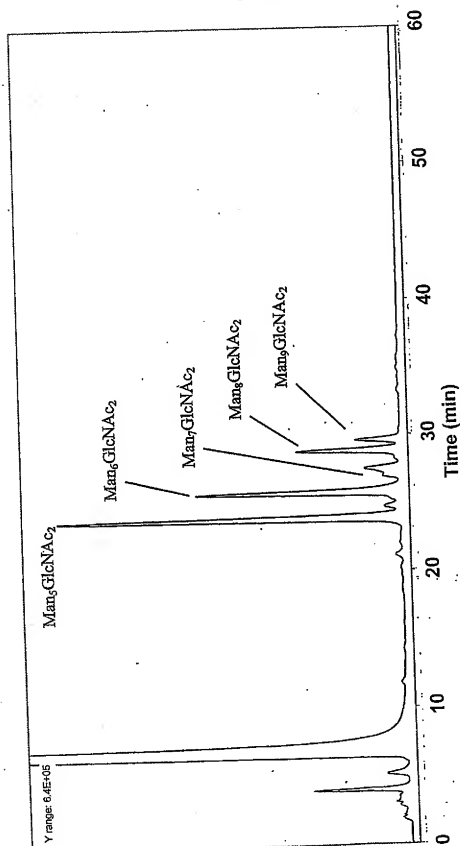


FIG. 92B



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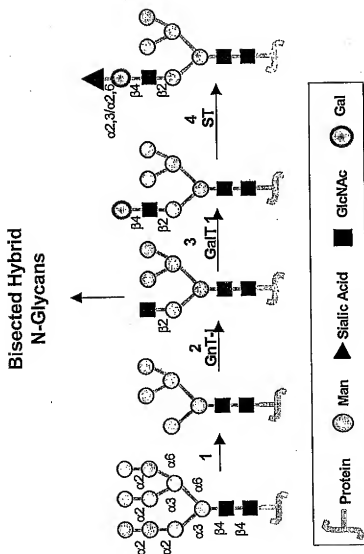
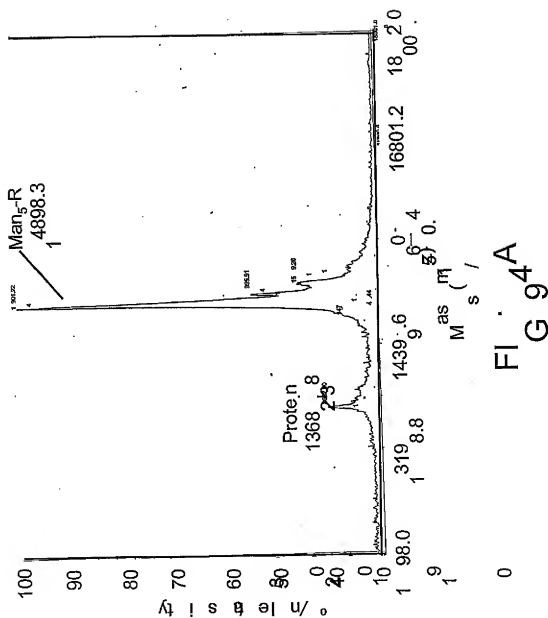
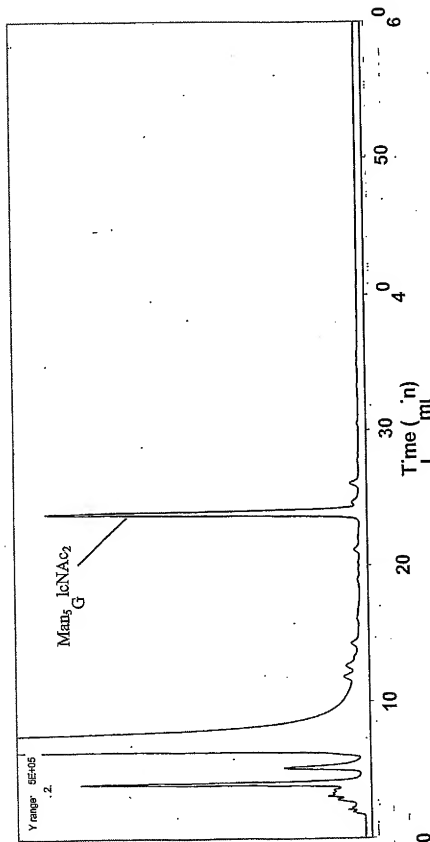


FIG. 93

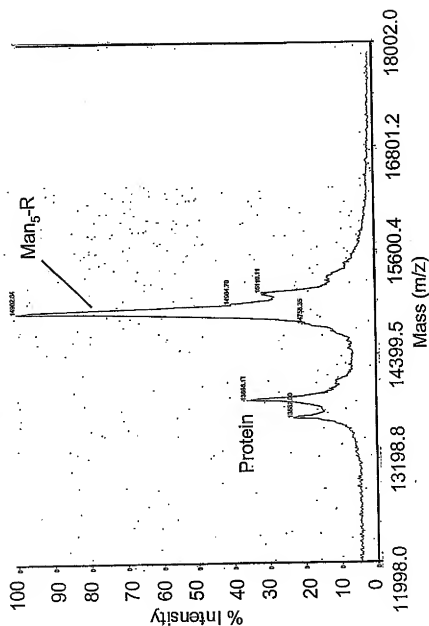
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F 94B  
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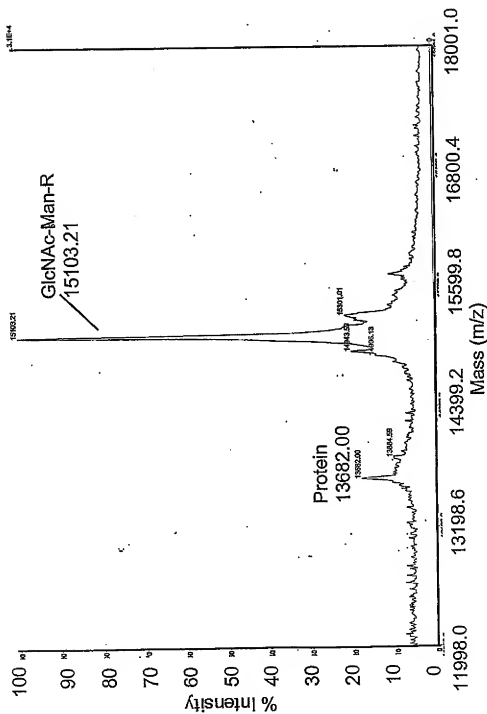


FIG. 96

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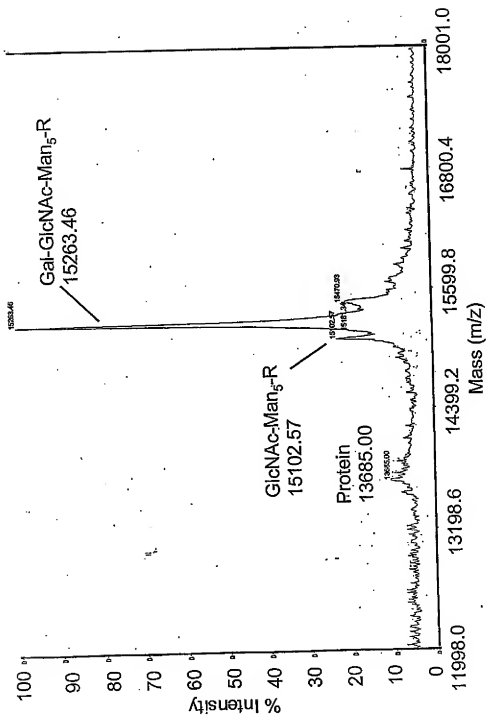


FIG. 97

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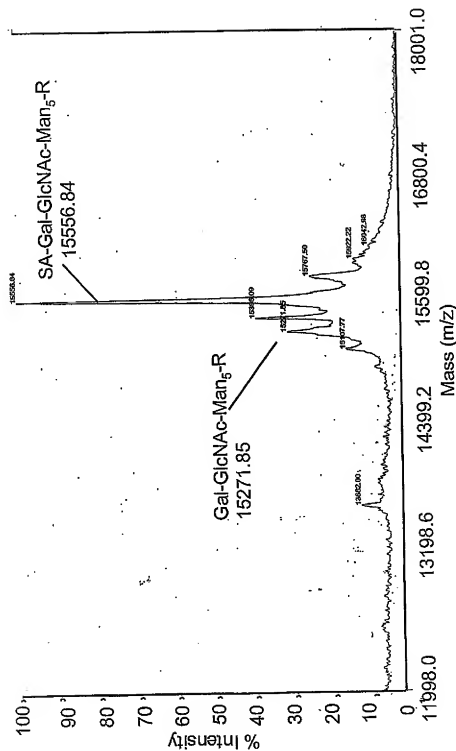


FIG. 98

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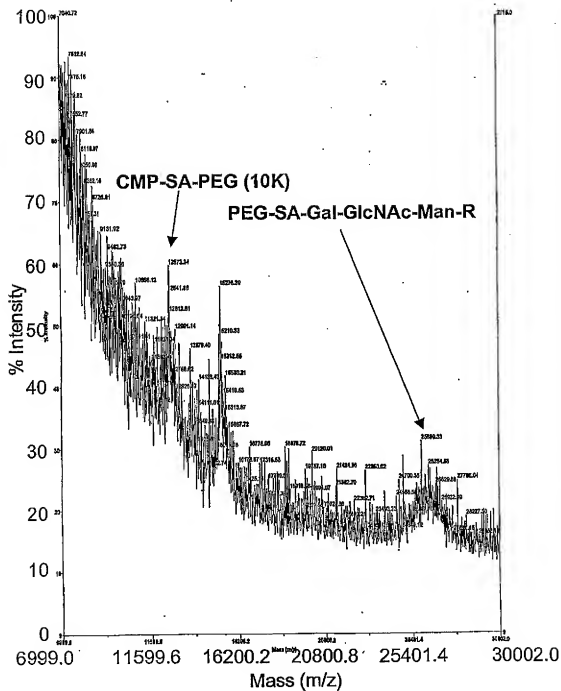


FIG. 99A





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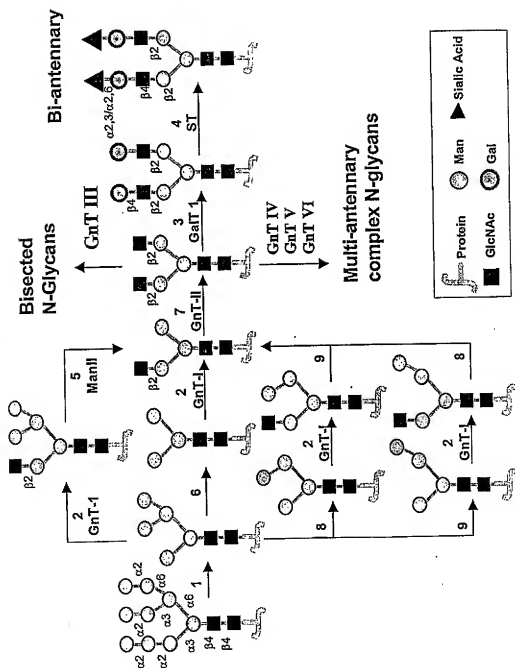


FIG. 100

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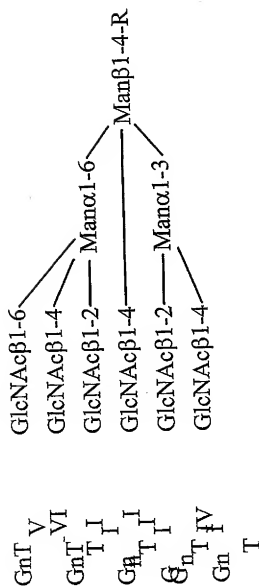


FIG. 101

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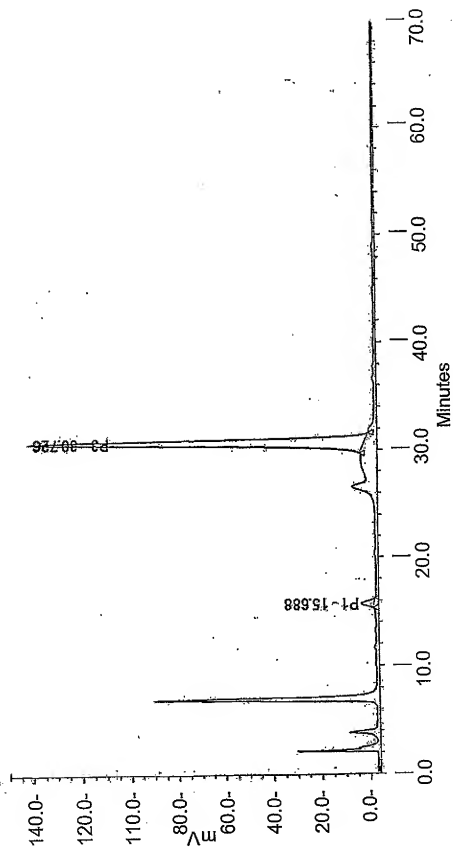


FIG. 102A

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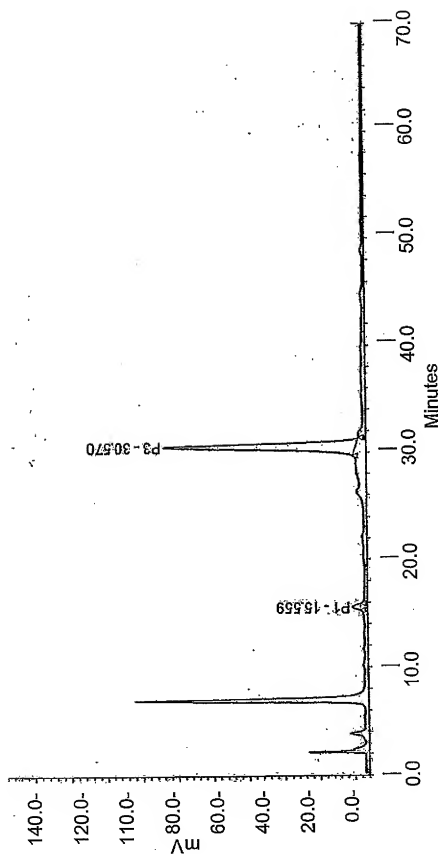


FIG. 102B

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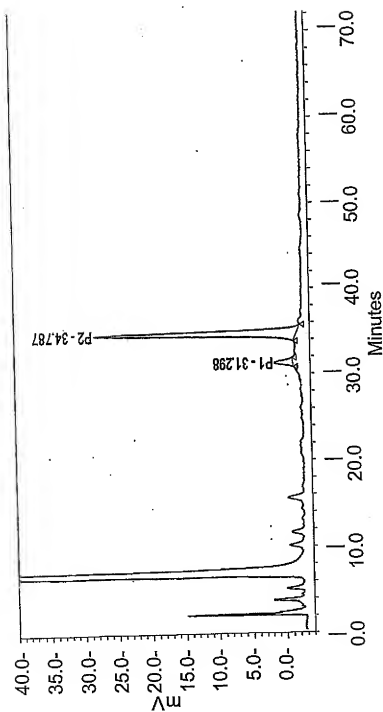


FIG. 103

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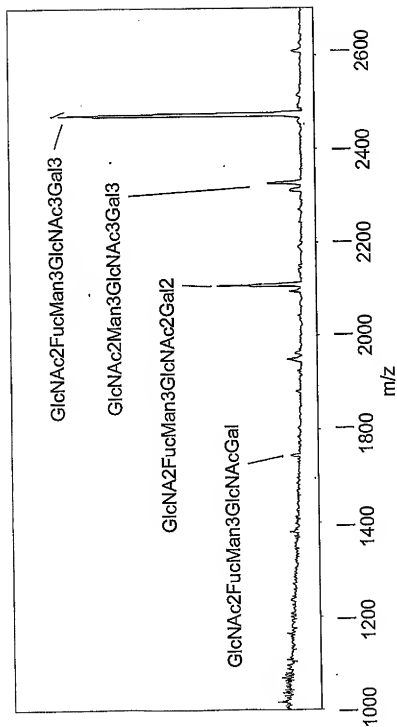


FIG. 104

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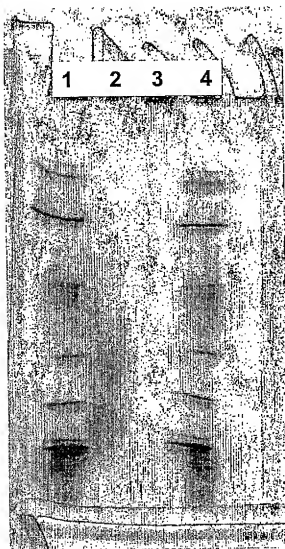


FIG. 105



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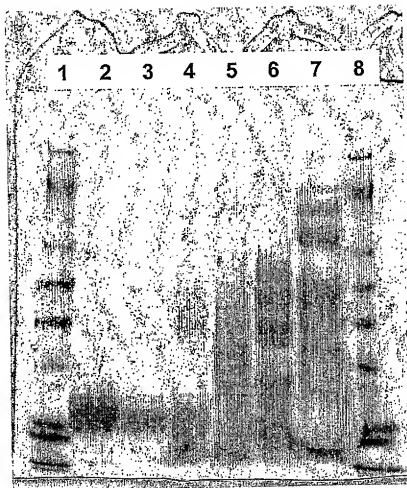


FIG. 106

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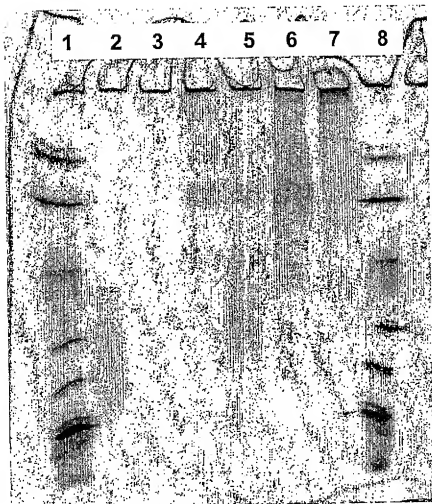


FIG. 107

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FIG. 108

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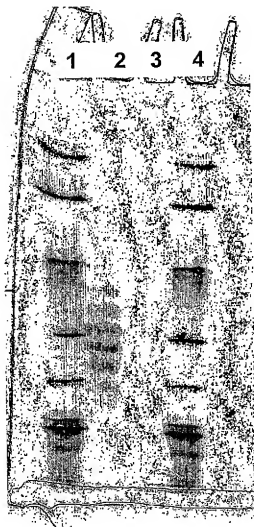


FIG. 109

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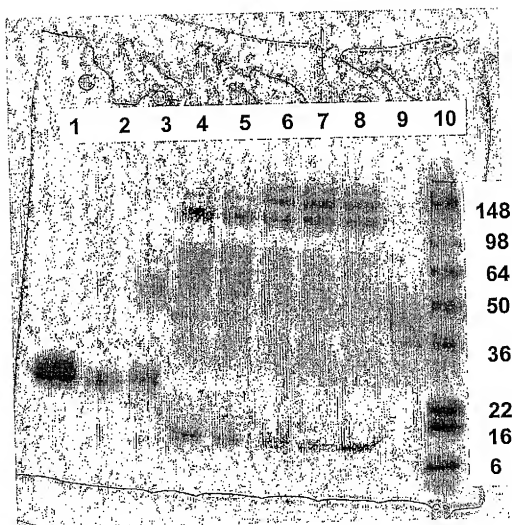


FIG. 110

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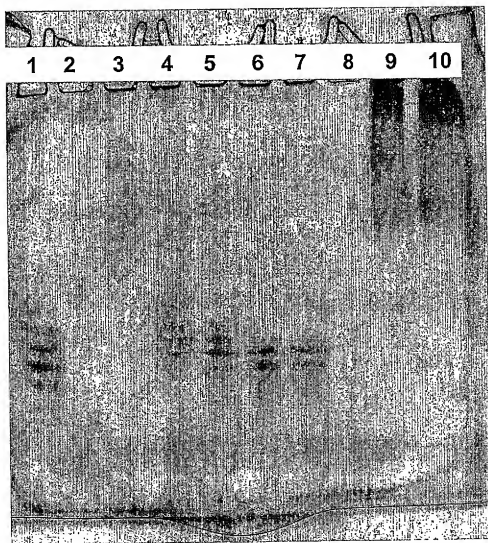
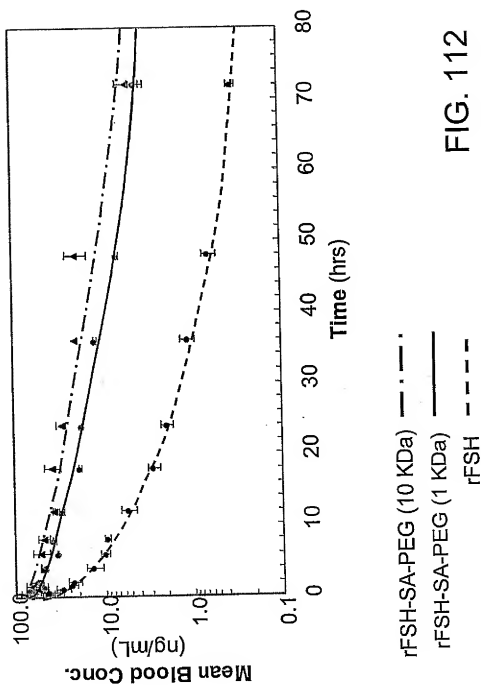


FIG. 111

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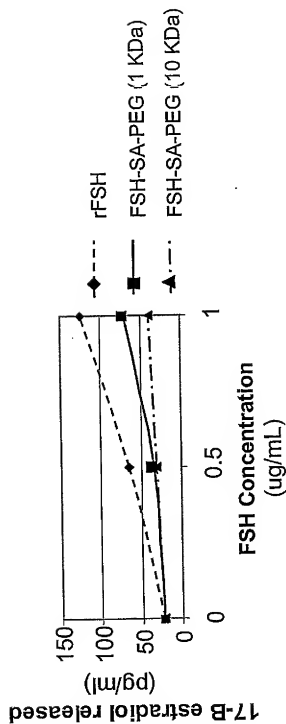


FIG. 113



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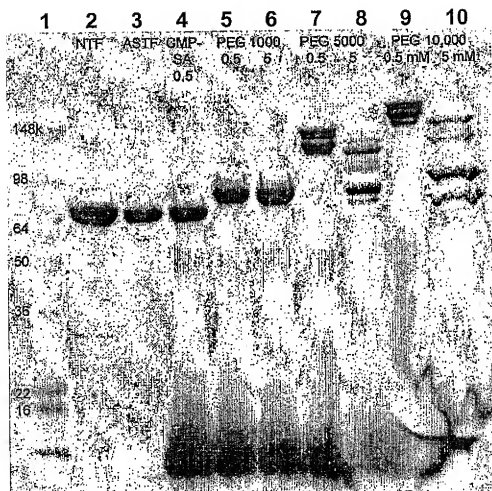


FIG. 114

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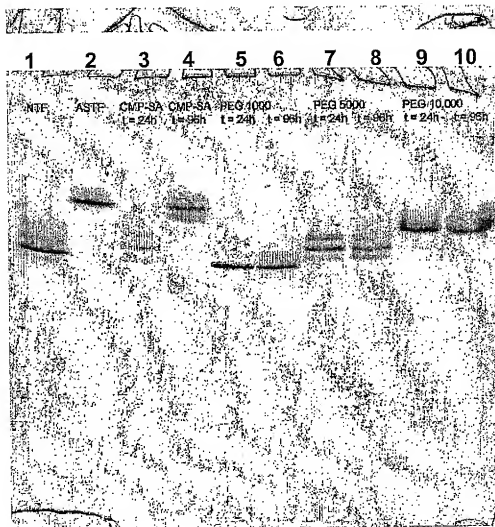


FIG. 115

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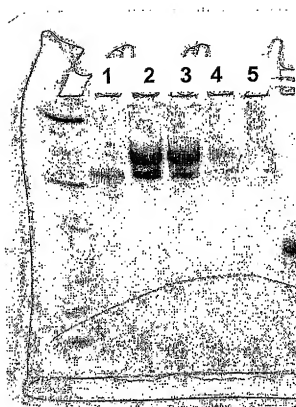


FIG. 116

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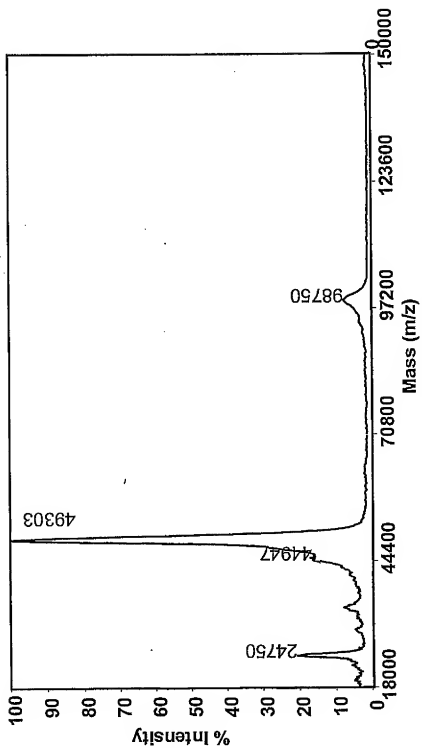


FIG. 117

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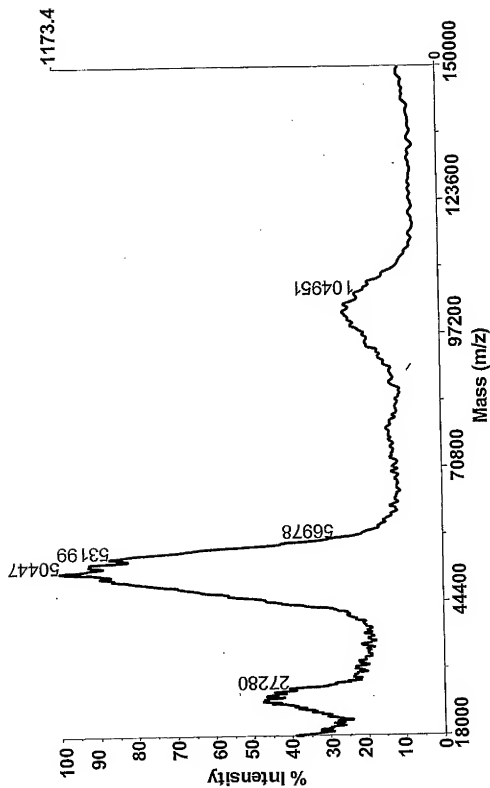


FIG. 118

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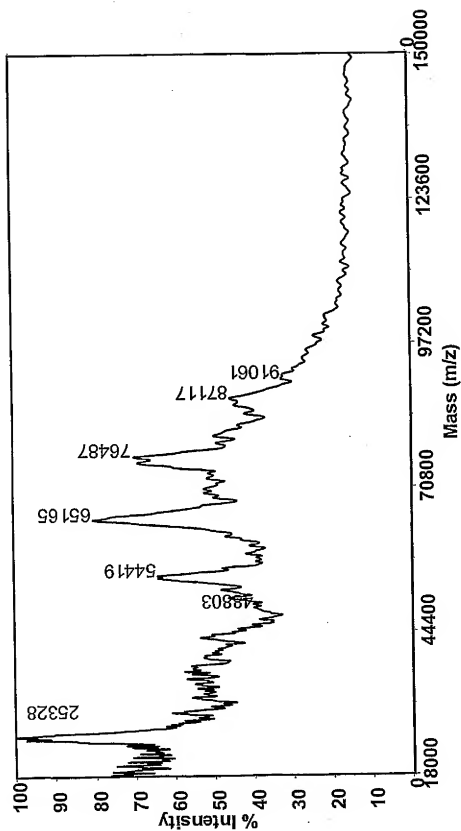


FIG. 119

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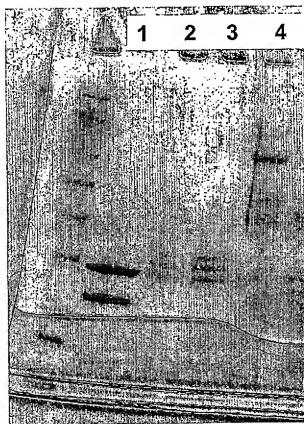


FIG. 120

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FIG. 121



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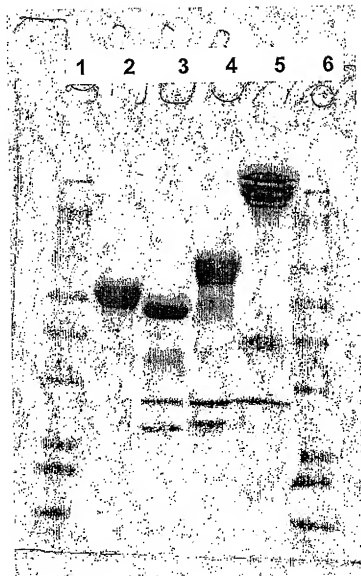


FIG. 122

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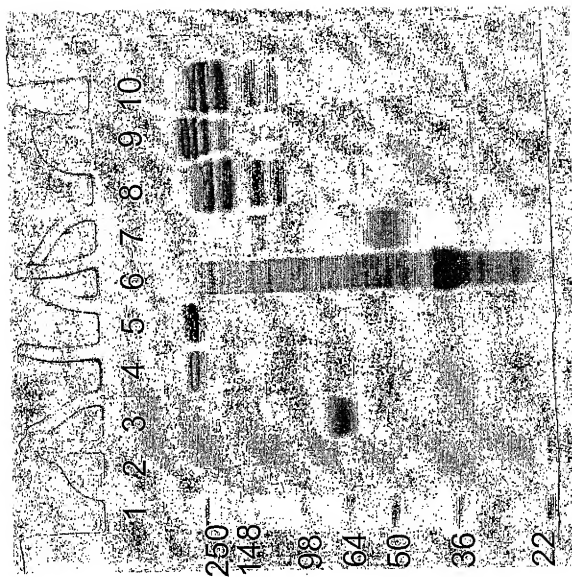


FIG. 123

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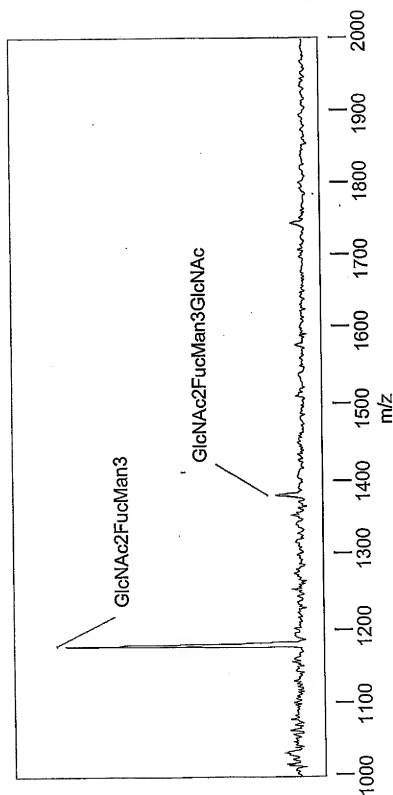


FIG. 124

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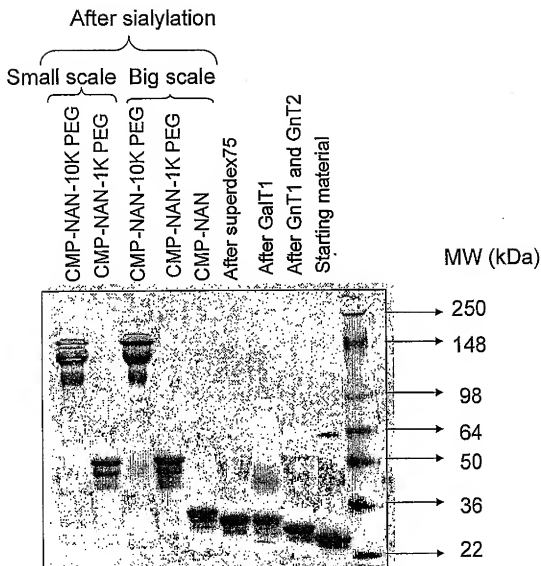


FIG. 125

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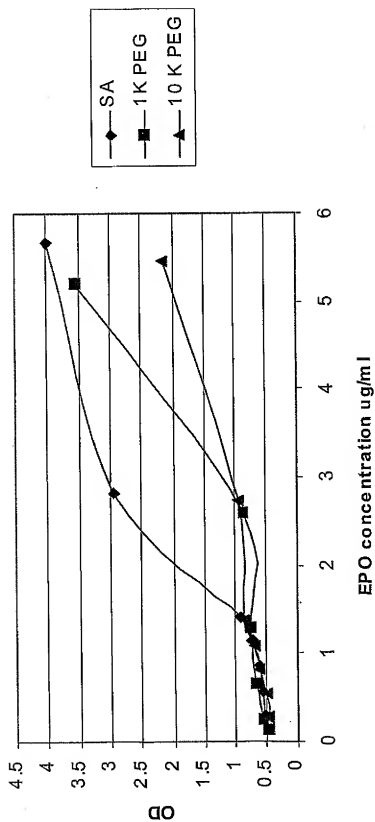


FIG. 126

## SEQUENCE LISTING

<110> Neose Technologies, Inc.  
 DeFrees, Shawn  
 Zopf, David  
 Bayer, Robert  
 Bowe, Caryn  
 Hakes, David  
 Chen, Xi

<120> REMODELING AND GLYCOCONJUGATION OF PEPTIDES

<130> 040853-01-5050WO

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<151> 2001-10-10

<150> US 60/344,692

<151> 2001-10-19

<150> US 60/334,233

<151> 2001-11-08

<150> US 60/334,301

<151> 2001-11-08

<150> US 60/387,292

<151> 2002-06-07

<150> US 60/391,777

<151> 2002-06-25

<150> US 60/396,594

<151> 2002-07-17

<150> US 60/404,249

<151> 2002-08-16

<150> US 60/407,527

<151> 2002-08-28

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 cccaccttgg acacactgca gctggacgtc gccgactttg ccaccaccat ctggcagcag 360  
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Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe

145

150

155

160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
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&lt;211&gt; 1733

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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tgcaataata aaacattaac ttatactttt ttaatttaat gtatagaata gagatataca      180
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&lt;210&gt; 4

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
1           5           10          15

```

```

Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
          20          25          30

```

```

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
          35          40          45

```

```

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
          50          55          60

```

```

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
          65          70          75          80

```

```

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
          85          90          95

```

```

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
          100          105          110

```

```

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
          115          120          125

```

```

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
          130          135          140

```

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro  
 145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu  
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu  
 180 185

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 <213> Homo sapiens

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 ctctctgtggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac 180  
 atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc 240  
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 cttacaggtt acctccgaaa ctgaagatct cctagcctgt cctctgggga ctggacaatt 600  
 gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca 660  
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<210> 6  
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 <212> PRT  
 <213> Homo sapiens

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Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser  
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Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg  
20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg  
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu  
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile  
65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser  
85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu  
115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys  
130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser  
145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr  
165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn  
180 185

<210> 7  
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gcgttctctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtcg 180  
tccttcgagg aggcccgga gatcttcaag gacgcggaga ggaogaagct gttctggatt 240

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gccccatttc cc

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<210> 8  
 <211> 444  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln  
 1 5 10 15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val  
 20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro  
 35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu  
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile  
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly  
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile  
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr  
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala  
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile  
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val  
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu  
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg  
225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly  
245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr  
260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln  
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg  
290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser  
305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met  
325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser  
340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala  
355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly  
370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val  
385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr  
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Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro  
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&lt;210&gt; 10

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

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Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
1           5           10           15

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Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20           25           30

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Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn  
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys  
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn  
 65 70 75 80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln  
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile  
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys  
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe  
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly  
 145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe  
 165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala  
 180 185 190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu  
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe  
 210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp  
 225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile  
 245 250 255



Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly  
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu  
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His  
 290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu  
 305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys  
 325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly  
 340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu  
 355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu  
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe  
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His  
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp  
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val  
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr  
 450 455 460

<210> 11  
 <211> 603  
 <212> DNA  
 <213> Homo sapiens

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<400> 11
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ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca      180
tatccactc cactaaggtc caagaagaag atgttggtcc aaaagaacgt cacctcagag      240
tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg      300
gagaaccaca ogcggtgcc ctcagctact tgttattatc acaaatotta aatgttttac      360
caagtgtgtg ctgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt      420
atggctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg      480
atactagcca gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct      540
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atc                                                                           603

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<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

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<400> 12

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Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1           5           10           15

```

```

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
          20           25           30

```

```

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
          35           40           45

```

```

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
          50           55           60

```

```

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65           70           75           80

```

```

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
          85           90           95

```

```

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
          100          105          110

```

Tyr His Lys Ser  
115

<210> 13  
<211> 390  
<212> DNA  
<213> Homo sapiens

<400> 13  
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tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcgttt ctgcataagc 120  
atcaacacca cttggtgtgc tggctactgc tacaccaggg atctggtgta taaggacca 180  
gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggatatga aacagtgaga 240  
gtgcccggt gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300  
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct gggggccagc 360  
tactgtctct ttggtgaaat gaaagaataa 390

<210> 14  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile  
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys  
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly  
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys  
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg  
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val  
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
 100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys  
 115 120 125

Glu

<210> 15  
 <211> 1342  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
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 gccccgggtg tggtcaccg gcgcgcccca ggctgctgag ggaccccgcc caggcgcgga 180  
 gatgggggtg cacgaatgtc ctgcttggtg gtgcttctc ctgtccctgc tgtgctccc 240  
 tctgggctc ccagctctgg gcgccccacc acgcctcctc tgtgacagcc gagtccctga 300  
 gaggtagctc ttggaggcca aggaggccga gaatatcac acgggctgtg ctgaacactg 360  
 cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420  
 gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480  
 tgtctgcgg ggcaggccc tgttggtcaa ctctcccg ccgtgggagc cctgcagct 540  
 gcatgtggt aaagccgtca gtggccttg cagcctcacc actctgctc gggctctcg 600  
 agccagaag gaagccatct cccctccaga tgcggcctca gtgctccac tccgaacaat 660  
 cactgtgac actttccgca aactcttccg agtctactcc aatttctc cgggaaagct 720  
 gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccaggtg tgtccacctg 780  
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 tcacagggac aacttgaggg ccagagcagc gaagcattca gagagcagct ttaactcag 1020  
 ggacagagcc atgctgggaa gacgcctgag ctactcggc accctgcaaa atttgatgcc 1080  
 aggacacgct ttggaggcga tttaacctgt ttgcaccta ccactcagga caggatgacc 1140

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tgggagaactt aggtgggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt 1200
ggtgggcaaga gccccttga caccgggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctgggt ctcctgggtt ccaagttttg tgtattcttc aacctcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

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<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

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<400> 16

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1           5           10           15

```

```

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
          20           25           30

```

```

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
          35           40           45

```

```

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
          50           55           60

```

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65           70           75           80

```

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
          85           90           95

```

```

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
          100          105          110

```

```

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
          115          120          125

```

```

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
          130          135          140

```

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
          145          150          155          160

```

```

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

```

165

170

175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp  
 180 185 190

Arg

<210> 17  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg 120  
 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180  
 tcagaaatgt ttgacctcca ggagccgacc tgcctacaga ccogcctgga gctgtacaag 240  
 cagggcctgc ggggcagcct caccaagctc aagggccctc tgaccatgat gccagccac 300  
 tacaagcagc actgccctcc aaccccgaa acttctctgt caaccagat tatcaccttt 360  
 gaaagtcca aagagaacct gaaggacttt ctgcttctga tcccccttga ctgctgggag 420  
 ccagtccagg agtga 435

<210> 18  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile  
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His  
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp  
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe  
 50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys  
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met  
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys  
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu  
130 135 140

<210> 19  
<211> 501  
<212> DNA  
<213> Homo sapiens

<400> 19  
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tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca 120  
ggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180  
gaggagagtg acagaaaaat aatgcagagc caaattgtct ctttttactt caaacttttt 240  
aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300  
aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360  
tattcggttaa ctgacttgaa tgccaacgc aaagcaatac atgaactcat ccaagtgatg 420  
gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480  
ggtcgaagag catccagta a 501

<210> 20  
<211> 166  
<212> PRT  
<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu  
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu

20

25

30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn  
 35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp  
 50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe  
 65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile  
 85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg  
 100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val  
 115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser  
 130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg  
 145 150 155 160

Gly Arg Arg Ala Ser Gln  
 165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

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 gacagataca tcccacatg atcaggatca cccaaccttc aacaagatca cccccaacct 180  
 ggctgagttc gccttcagcc tataccgcc gctggcacac cagtccaaca gcaccaatat 240  
 cttctctctc ccagtgagca tcgtctacgc ctttgcaatg ctctccttgg ggaccaaggc 300  
 tgacactcac gatgaaatcc tggagggcct gaatttcaac' ctcaoggaga ttcoggaggc 360



tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420  
 ccagctgacc accggcaatg gcctgttccct cagcgagggc ctgaagctag tggataagtt 480  
 tttggaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact tcggggacac 540  
 cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt 600  
 ggatttggtc aaggagcttg acagagacac agtttttgct ctgggtgaatt acatcttctt 660  
 taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720  
 ggaccagggt accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca 780  
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 actgtccatt actggaacct atgatctgaa gagcgtcctg ggtcaactgg gcatcactaa 1020  
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 catgttttta gaggccatcc ccatgtctat cccccccgag gtcaagtcca acaaacctt 1200  
 tgtcttctta atgattgaac aaaataccaa gtctccccct tcatgggaa aagtggtgaa 1260  
 tccccccaa aaataactgc ctctcgctcc tcaaccctc ccctccatcc ctggcccccct 1320  
 ccctggatga cattaaagaa ggggttgagct gg 1352

<210> 22  
 <211> 418  
 <212> PRT  
 <213> Homo sapiens

<400> 22

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys  
 1 5 10 15

Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala  
 20 25 30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn  
 35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln  
 50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser  
 65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr  
 85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro  
 100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn  
 115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu  
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
 145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
 165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
 180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
 195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val  
 225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
 245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
 260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
 275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr  
 405 410 415

Gln Lys

<210> 23  
 <211> 2004  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
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 ctctatcctt cagagactct ggaacccctg tggctctctc ttcactcaat gaccctgagg 120  
 ggatggagtt ttcaagtctt tccagagagg aatgtcccaa gcctttgagt agggtaaaga 180  
 tcatggctgg cagcctcaca ggtttgcttc tacttcaggc agtgcgtggt gcatcagggtg 240  
 ccgcgccctg catccctaaa agcttcgggt acagctcggg ggtgtgtgtc tgcaatgcca 300  
 catactgtga ctcccttgac ccccgacct ttccctgcct tggtacctc agccgctatg 360  
 agagtacag cagtggggga cggatggagc tgagtatggg gcccatccag gctaatacaca 420  
 cgggcacagg cctgctactg acctgcagc cagaacagaa gtccagaaa gtgaagggat 480

btggaggggc catgacagat gctgctgctc tcaacatcct tgccctgtca cccctgtccc	540
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taccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg	660
atttccagtt gcacaacttc agcctcccag aggaagatac caagctcaag atacccttga	720
ttcaccgagc cctgcagttg gccagcgtc ccgttttact ccttgccagc ccttggacat	780
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ccggagacat ctaccaccag acctgggcca gatactttgt gaagttcctg gatgcctatg	900
ctgagcaca gttacagttc tgggcagtg cagctgaaaa tgagccttct gctgggctgt	960
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tggatgacca acgcttctg ctgcccact gggcaaaagt ggtactgaca gaccagaag	1140
cagctaaata tgttcatggc attgtgtac attggtacct ggactttctg gctccagcca	1200
aagccacct aggggagaca caccgctgt tcccacaac catgtcttt gccatcaggg	1260
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tgagtagcag ccacagcacc atcacgaacc tctgtacca tgggtctggc tggaccgact	1380
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ccatcattgt agacatcacc aaggacacgt tttaaaaaa gcccatgttc taccaccttg	1500
gccacttcag caagttcatt cctgagggt cccagagagt ggggtgggt gccagtcaga	1560
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gatactcaag gaggcacttg gctcagcctg ggcattaaa ggacagagtc agctcacacg	1800
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ggggcaatgg tttgggtgac tcactttccc ctctaggtgg tgcccagggc tggaggcccc	1920
tagaaaaaga tcagtaagcc ccagtgtccc cccagcccc atgcttatgt gaacatgcgc	1980
tgtgtgctgc ttgctttgga aact	2004

<210> 24  
 <211> 536  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser  
 1 5 10 15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Gln  
 20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe  
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser  
 50 55 60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu  
 65 70 75 80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln  
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala  
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu  
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val  
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp  
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp  
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln  
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu

210	215	220
Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro 225 230 235 240		
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu 245 250 255		
Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu 260 265 270		
Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu 275 280 285		
Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly 290 295 300		
Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu 305 310 315 320		
Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr 325 330 335		
Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Tyr Tyr 340 345 350		
Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg 355 360 365		
Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser 370 375 380		
Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met 385 390 395 400		
Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly 405 410 415		
Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp 420 425 430		
Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp 435 440 445		

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
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Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys  
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Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val  
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Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys  
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Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile  
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His Thr Tyr Leu Trp His Arg Gln  
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&lt;210&gt; 26

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg  
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Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met  
 35 40 45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn  
 50 55 60



Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser  
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Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr  
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Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu  
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Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr  
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Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser  
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Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro  
 145 150 155 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His  
 165 170 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val  
 180 185 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys  
 195 200 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg  
 210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn  
 225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala  
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Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly  
 260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp  
 275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr

290

295

300

Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala  
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Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro  
325 330 335

Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile  
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Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu  
355 360 365

Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu  
370 375 380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp  
385 390 395 400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser  
405 410 415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro  
420 425 430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly  
435 440 445

Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
450 455 460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His  
465 470 475 480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr  
485 490 495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp  
500 505 510

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val  
515 520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly  
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Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met  
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Arg Pro

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 <212> DNA  
 <213> Homo sapiens

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 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<400> 28

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Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr	50	55	60
Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln	65	70	75
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala	85	90	95
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile	100	105	110
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys	115	120	125
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp	130	135	140
Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr	145	150	155

&lt;210&gt; 29

&lt;211&gt; 7931

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

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 ttgttgaaag ctttgaaata aaataacaat gtcttcttga aatttgtgat ggccaagaaa 7920  
 gaaaatgatg a 7931

&lt;210&gt; 30

&lt;211&gt; 2351

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe  
 1 5 10 15

Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser  
 20 25 30

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg  
 35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val  
 50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile  
 65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln  
 85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser  
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser  
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp  
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu  
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser  
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile  
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr  
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly  
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp  
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr  
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val  
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile  
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser  
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met  
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His  
 325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro  
 340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp  
 355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser  
 370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr  
 385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro  
 405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
 420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met  
 435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu  
 450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu  
 465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro  
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys  
 500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe  
 515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp  
 530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg

545	550	555	560
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu	565	570	575
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val	580	585	590
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu	595	600	605
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp	610	615	620
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val	625	630	635
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp	645	650	655
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe	660	665	670
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr	675	680	685
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro	690	695	700
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly	705	710	715
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp	725	730	735
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys	740	745	750
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg	755	760	765
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp	770	775	780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys  
 785 790 795 800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser  
 805 810 815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr  
 820 825 830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn  
 835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly  
 850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu  
 865 870 875 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys  
 885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn  
 900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met  
 915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys  
 930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu  
 945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu  
 965 970 975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe  
 980 985 990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala  
 995 1000 1005

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser  
 1010 1015 1020

Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser  
 1025 1030 1035

Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu  
 1040 1045 1050

Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg  
 1055 1060 1065

Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met  
 1070 1075 1080

Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln  
 1085 1090 1095

Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met  
 1100 1105 1110

Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile  
 1115 1120 1125

Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro  
 1130 1135 1140

Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu  
 1145 1150 1155

Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys  
 1160 1165 1170

Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro  
 1175 1180 1185

Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu  
 1190 1195 1200

Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu  
 1205 1210 1215

Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile  
 1220 1225 1230  
 His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu  
 1235 1240 1245  
 Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr  
 1250 1255 1260  
 Ala Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn  
 1265 1270 1275  
 Arg Thr Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu  
 1280 1285 1290  
 Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu  
 1295 1300 1305  
 Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln  
 1310 1315 1320  
 Asn Phe Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg  
 1325 1330 1335  
 Leu Pro Leu Glu Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp  
 1340 1345 1350  
 Asp Thr Ser Thr Gln Trp Ser Lys Asn Met Lys His Leu Thr Pro  
 1355 1360 1365  
 Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu Lys Gly Ala  
 1370 1375 1380  
 Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser  
 1385 1390 1395  
 Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser  
 1400 1405 1410  
 Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe  
 1415 1420 1425  
 Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys

1430	1435	1440
Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys 1445 1450 1455		
Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly 1460 1465 1470		
Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser 1475 1480 1485		
Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp 1490 1495 1500		
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His 1505 1510 1515		
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser 1520 1525 1530		
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr 1535 1540 1545		
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val 1550 1555 1560		
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser 1565 1570 1575		
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln 1580 1585 1590		
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys 1595 1600 1605		
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys 1610 1615 1620		
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys 1625 1630 1635		
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg 1640 1645 1650		



Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu  
 1655 1660 1665  
 Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr  
 1670 1675 1680  
 Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile  
 1685 1690 1695  
 Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys  
 1700 1705 1710  
 Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr  
 1715 1720 1725  
 Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser  
 1730 1735 1740  
 Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr  
 1745 1750 1755  
 Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu  
 1760 1765 1770  
 His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp  
 1775 1780 1785  
 Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser  
 1790 1795 1800  
 Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly  
 1805 1810 1815  
 Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr  
 1820 1825 1830  
 Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu  
 1835 1840 1845  
 Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu  
 1850 1855 1860

Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His  
 1865 1870 1875  
 Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln  
 1880 1885 1890  
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp  
 1895 1900 1905  
 Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn  
 1910 1915 1920  
 Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His  
 1925 1930 1935  
 Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met  
 1940 1945 1950  
 Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser  
 1955 1960 1965  
 Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr  
 1970 1975 1980  
 Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr  
 1985 1990 1995  
 Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly  
 2000 2005 2010  
 Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly  
 2015 2020 2025  
 Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro  
 2030 2035 2040  
 Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala  
 2045 2050 2055  
 Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His  
 2060 2065 2070

Tyr Ser	Gly Ser	Ile Asn	Ala	Trp Ser	Thr Lys	Glu	Pro Phe	Ser
2075			2080				2085	
Trp Ile	Lys Val	Asp Leu	Leu	Ala Pro	Met Ile	Ile	His Gly	Ile
2090			2095				2100	
Lys Thr	Gln Gly	Ala Arg	Gln	Lys Phe	Ser Ser	Leu	Tyr Ile	Ser
2105			2110				2115	
Gln Phe	Ile Ile	Met Tyr	Ser	Leu Asp	Gly Lys	Lys	Trp Gln	Thr
2120			2125				2130	
Tyr Arg	Gly Asn	Ser Thr	Gly	Thr Leu	Met Val	Phe	Phe Gly	Asn
2135			2140				2145	
Val Asp	Ser Ser	Gly Ile	Lys	His Asn	Ile Phe	Asn	Pro Pro	Ile
2150			2155				2160	
Ile Ala	Arg Tyr	Ile Arg	Leu	His Pro	Thr His	Tyr	Ser Ile	Arg
2165			2170				2175	
Ser Thr	Leu Arg	Met Glu	Leu	Met Gly	Cys Asp	Leu	Asn Ser	Cys
2180			2185				2190	
Ser Met	Pro Leu	Gly Met	Glu	Ser Lys	Ala Ile	Ser	Asp Ala	Gln
2195			2200				2205	
Ile Thr	Ala Ser	Ser Tyr	Phe	Thr Asn	Met Phe	Ala	Thr Trp	Ser
2210			2215				2220	
Pro Ser	Lys Ala	Arg Leu	His	Leu Gln	Gly Arg	Ser	Asn Ala	Trp
2225			2230				2235	
Arg Pro	Gln Val	Asn Asn	Pro	Lys Glu	Trp Leu	Gln	Val Asp	Phe
2240			2245				2250	
Gln Lys	Thr Met	Lys Val	Thr	Gly Val	Thr Thr	Gln	Gly Val	Lys
2255			2260				2265	
Ser Leu	Leu Thr	Ser Met	Tyr	Val Lys	Glu Phe	Leu	Ile Ser	Ser
2270			2275				2280	
Ser Gln	Asp Gly	His Gln	Trp	Thr Leu	phe Phe	Gln	Asn Gly	Lys

2285                      2290                      2295

Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val  
2300                      2305                      2310

Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His  
2315                      2320                      2325

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu  
2330                      2335                      2340

Gly Cys Glu Ala Gln Asp Leu Tyr  
2345                      2350

<210> 31  
<211> 1471  
<212> DNA  
<213> Homo sapiens

<400> 31  
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cacgccttgc ccgccacggt gccatttaca ccctaogccc oggagcccg gagcacatgc 120  
oggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctgcgcgggc 180  
caacatgcaa aagtcttctg taccaagacc toggacaccg tgtgtgactc ctgtgaggac 240  
agcacatata ccagctctg gaactgggtt ccgagtgct tgagctgtgg ctcccgcgtg 300  
agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcac ctgcacctgc 360  
aggcccggt ggtactgcgc gctgagcaag caggaggggt gccggtgtg cgcgcgcgtg 420  
cgcaagtgc gcccgggctt cggcgtggcc agaccaggaa ctgaaacac agacgtgtgtg 480  
tgcaagccct gtgcgccggg gaogttctcc aacacgaact catccacgga tatttgcagg 540  
ccccaccaga tctgtaactg ggtggccatc cctgggaatg caagcatgga tgcagtctgc 600  
acgtccactg ccccccaccc gagtatggcc ccaggggcag tacacttacc ccagccagtg 660  
tccacacgat cccaacacac gcagccaact ccagaaccca gcaactgctcc aagcacctcc 720  
ttctctgctc caatggggcc cagccccca gctgaaggga gcaactggcga cttcgtcttt 780  
ccagttggac tgatttggg tgtgacagcc ttgggtctac taataatagg agtggtgaa 840  
tgtgtcatca tgaccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaagtg 900  
cctcacttgc ctgcgcgataa ggcccggggt acacagggcc ccgagcagca gcacctgctg 960

atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020  
 agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggccagtgg ggcgggggag 1080  
 gcccgggcca gcaccgggag ctcaattctt tcccctgggt gccatgggac ccagggtcaat 1140  
 gtcacctgca tcgtgaacgt ctgtagcagc tctgaccaca gtcacagtgc ctctcccaa 1200  
 gccagctcca caatgggaga cacagattcc agccctcgg agtcccga gacgagcag 1260  
 gtcccttctt ccaaggagga atgtgccttt cggtcacagc tggagacgcc agagaccctg 1320  
 ctggggagca ccgaagagaa gcccctgccc ctggagtgcc ctgatgctgg gatgaagccc 1380  
 agttaaccag gccggtgtgg gctgtgtcgt agccaagtg ggctgagccc tggcaggatg 1440  
 accctgcgaa ggggccctgg tcctccagg c 1471

<210> 32  
 <211> 461  
 <212> FRT  
 <213> Homo sapiens

<400> 32

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
 1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser  
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly  
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly  
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys  
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro  
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser  
 325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly  
 340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser  
355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile  
370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln  
385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro  
405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser  
420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro  
435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser  
450 455 460

<210> 33  
<211> 1475  
<212> DNA  
<213> Homo sapiens

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tcgtgagcga ctccaaggc agcaatgaac ttcattcaagt tccatcgaac tgtgactgtc 180  
taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240  
caagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300  
atggtcactt ttaccgagga aaggccagca ctgacaccat gggcgggccc tgccctgccct 360  
ggaactctgc cactgtcctt cagcaaactg accatgccca cagatctgat gctcttcagc 420  
tggtcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctgggtgt 480  
atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcgt ggtgcagtgc tgcgcagatg 540  
gaaaaaagc ctcctctcct ccagaagaat taaaatttca gtgtggccaa aagactctga 600  
ggccccgctt taagattatt gggggagaat tcaccacat cgagaaccag ccctgggttg 660  
cgcccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720

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tcagcccttg ctgggtgatac agcgccacac actgcttcat tgattacca aagaaggagg      780
actacatcgt ctacctgggt cgctcaaggc ttaactcaa caccgaagg gagatgaagt      840
ttgaggtgga aaacctatc ctacacaagg actacagcgc tgacaagctt gctcaccaca      900
acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga      960
ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg     1020
agatcactgg ctttggaata gagaattcta ccgactatct ctatccggag cagctgaaga     1080
tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg     1140
aagtcaccac caaaatgctg tgtgtgctg acccacagt gaaaacagat tcctgccagg     1200
gagactcagg gggaccctc gtctgttccc tccaaggccg catgactttg actggaattg     1260
tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac     1320
acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg     1380
ccccagggag gaaacgggca ccaccgctt tcttgctggg tgtcattttt gcagtagagt     1440
catctccatc agctgtaaga agagactggg aagat                                  1475

```

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<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

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<400> 34
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Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1           5           10           15

```

```

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
          20           25           30

```

```

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
          35           40           45

```

```

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
          50           55           60

```

```

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65           70           75           80

```

```

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
          85           90           95

```



Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp  
180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val  
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His  
210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly  
225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val  
245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His  
260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys  
275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr  
290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
305 310 315 320

Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val  
 325 330 335

Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly  
 340 345 350

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys  
 355 360 365

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu  
 370 375 380

Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys  
 385 390 395 400

Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu  
 405 410 415

Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu  
 420 425 430

<210> 35  
 <211> 107  
 <212> PRT  
 <213> Mus musculus

<400> 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala  
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 36  
<211> 120  
<212> PRT  
<213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr  
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 37  
<211> 120  
<212> PRT  
<213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser  
                   20                                  25                                  30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu  
                   35                                  40                                  45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser  
                   50                                  55                                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val  
                   65                                  70                                  75                                  80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
                                   85                                  90                                  95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala  
                   100                                  105                                  110

Gly Thr Thr Val Thr Val Ser Ser  
                   115                                  120

<210> 38  
 <211> 106  
 <212> PRT  
 <213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
   1                                  5                                  10                                  15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met  
                   20                                  25                                  30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr  
                   35                                  40                                  45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
                   50                                  55                                  60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp  
   65                                  70                                  75                                  80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr  
                   85                                  90                                  95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 39  
<211> 1039  
<212> DNA  
<213> Homo sapiens

<400> 39  
tctgtcacag gcagtgacct gaagtgtctc ttcagagacc tttcttcata gactactttt 60  
ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120  
cattctcgtc atctctgagg acatcaccaat catctcagga tgaggggcat gaagctgctg 180  
ggggcgctgc tggcactggc ggcctactcg cagggggcgg tgtccctgaa gatcgcagcc 240  
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccacctcgt cagctacatt 300  
gtgcagatcc tgagccgcta tgacatgcc ctggtccagg aggtcagaga cagccacctg 360  
actgcctggt ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420  
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480  
cctgaccagg tgtctgoggt ggacagctac tactacgatg atggctgoga gccctgcggg 540  
aacgacacct tcaacogaga gccagccatt gtcaggttct tctccgggtt cacagaggtc 600  
agggagtttg ccattgttcc cctgcatgcg gcccggggg acgcagtagc cgagatcgac 660  
gctctctatg acgtctacct ggatgtccaa gagaatggg gcttgaggga cgtcatgttg 720  
atgggcgact tcaatgcggg ctgcagctat gtgagacctc ccagtggtc atccatccgc 780  
ctgtggacaa gcccaccett ccagtggctg atccccgaca gcgtgacac cacagctaca 840  
cccacgcact gtgcctatga caggatcggt gttgcaggga tgcgtctcg aggcgcggtt 900  
gttcccgact oggctcttcc cttaacttc caggctgcct atggcctgag tgaccaactg 960  
gcccagcca tcagtacaa ctatccagtg gaggtgatgc tgaagtgage agccctccc 1020  
cacaccagtt gaactgcag 1039

<210> 40  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu

1	5	10	15
Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr	20	25	30
Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val	35	40	45
Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp	50	55	60
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp	65	70	75
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn	85	90	95
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser	100	105	110
Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn	115	120	125
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe	130	135	140
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly	145	150	155
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val	165	170	175
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn	180	185	190
Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu	195	200	205
Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr	210	215	220
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly	225	230	235
			240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
 245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
 260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys  
 275 280

<210> 41  
 <211> 678  
 <212> DNA  
 <213> Mus musculus

<400> 41  
 gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60  
 ttctcctgca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaaagaaca 120  
 aatggttctc caaggtctct cataaagtat gcttctgagt ctatgtctgg gatcccttc 180  
 aggttttagtg gcagtggtac agggacagat ttactctta gcatcaacac tgtggagtc 240  
 gaagatatgg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300  
 gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360  
 cctggaggat ccatgaaact ctctgtggtt gcctctggat tcattttcag taaccactgg 420  
 atgaactggg tccgccagtc tccagagaag ggccttgagt gggttgctga aattagatca 480  
 aaatctatta attctgcaac acattatgag gactctgtga aaggagggtt caccatctca 540  
 agagatgatt ccaaaagtc tgtctacctg caaatgaccg acttaagaac tgaagacact 600  
 ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggg 660  
 accactctca cagtctcc 678

<210> 42  
 <211> 226  
 <212> PRT  
 <213> Mus musculus

<400> 42

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly  
 1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile  
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser  
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe  
85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu  
100 105 110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser  
115 120 125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val  
130 135 140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser  
145 150 155 160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg  
165 170 175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met  
180 185 190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn  
195 200 205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
210 215 220

Val Ser  
225

<210> 43  
<211> 450



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

```

<400> 43
gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc      60
gectcctgcc cctgctggcg ctgctggccc tctggggacc tgaccagcc gcagcctttg      120
tgaaccaaca cctgtggggc tcacacctgg tggaaagtct ctacctagtg tgcgggggaa      180
gaggtcttct ctacacaccc aagaccggcc gggaggcaga ggacctgcag gtggggcagg      240
tggagctggg cggggggccct ggtgcaggca gctgcagcc cttggccctg gaggggctcc      300
tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg      360
agaactactg caactagacg cagcccgag gcagccccc acccgccgcc tctgcaccg      420
agagagatgg aataaagccc ttgaaccagg      450

```

&lt;210&gt; 44

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

```

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1           5           10          15

```

```

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
20          25          30

```

```

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
35          40          45

```

```

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
50          55          60

```

```

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65          70          75          80

```

```

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
85          90          95

```

```

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
100         105         110

```

&lt;210&gt; 45

<211> 1203  
 <212> DNA  
 <213> Hepatitis B virus

<400> 45  
 atgggaggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttctc tgttcccaat 60  
 cctctgggat tctttccga tcaccagttg gacctgcgt tcggagccaa ctcaacaat 120  
 ccagattggg aottcaacc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180  
 ggagacttcg ggcagggtt cccccacca caggcggtc tttgggggtg gagccctcag 240  
 gctcaggga tattgacaac agtgccagc gcgcctctc ctgtttccac caatcggcag 300  
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcctcc tcaggccatg 360  
 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagtgcg gggcctatat 420  
 tttctctctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgtctcacc 480  
 atatctgcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca 540  
 ggattcttag gacctctgct cgtgttacag gcgggggttt tctgttgac aagaatctc 600  
 acaataccac agagtctaga ctctgtgtg acttctctca atttcttagg gggagcacc 660  
 acgtgtctctg gccaaaattc gcagtcacca acctccaac actcaccaac ctcttctct 720  
 ccaatttgct ctggttatcg ctggatgtgt ctgcgggctt ttatcatatt cctcttcatc 780  
 ctgctcttat gctcatctt ctgtgtggtt ctctggact accaaggatg gttgcccgtt 840  
 tgtctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900  
 cctgctcaag gaacctctat gtttccctct tgtgtctgta caaaaccttc ggacggaaac 960  
 tgcaattgta ttcccatccc atcatctgg gctttcgcaa gattctatg ggagtgggcc 1020  
 tcagtccgtt tctctgggt cagtttacta gtgccatttg ttcagtgggt cgcagggtt 1080  
 tcccactcg tttggcttct agttatatgg atgatgtgtt attgggggcc aagtctgtac 1140  
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacat 1200  
 tga 1203

<210> 46  
 <211> 400  
 <212> PRT  
 <213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu  
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro  
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn  
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly  
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln  
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser  
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu  
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His  
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly  
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro  
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu  
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly  
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly  
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro  
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile  
245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu  
260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser  
275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly  
290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu  
325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro  
340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val  
355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser  
370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile  
385 390 395 400

<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

cgaccactc agggctctgt ggacagctca cctagctgca atggctacag gctcccgga	60
gtccctgtct ctgggttttg gctgctctg cctgccttg cttcaagagg gcagtgcctt	120
cccaaccatt cccttatcca gcccttttga caacgctatg ctccggcccc atcgtctgca	180
ccagctggcc tttagacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa	240
gtattcatte ctgcagaacc ccagacctc cctctgtttc tcagagtcta ttccgacacc	300

```

ctccaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct 360
gctcatccag tcgtggctgg agcccgctga gttcctcagg agtgtcttcg ccaacagcct 420
ggtgtacggc gctctcgaca gcaacgtcta tgacctccta aaggacctag aggaaggcat 480
ccaaacgctg atggggaggc tggaagatgg cagccccggg actgggcaga tcttcaagca 540
gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600
gctgctctac tgcttcagga aggacatgga caaggtcgag acattcctgc gcatcgcgca 660
gtgcgcgtct gtggagggca gctgtggctt ctacgtgccc ggggtggcatc cctgtgaccc 720
ctccccagtg cctctcctgg ccctggaagt tgccactcca gtgcccacca gccttgcctc 780
aataaaatta agttgcatc 799

```

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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

```

```

<400> 48

```

```

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1           5           10          15

```

```

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
          20          25          30

```

```

Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
          35          40          45

```

```

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
          50          55          60

```

```

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65          70          75          80

```

```

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
          85          90          95

```

```

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
          100          105          110

```

```

Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
          115          120          125

```

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu  
 130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg  
 145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser  
 165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe  
 180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys  
 195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe  
 210 215

<210> 49  
 <211> 963  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 atggagacag acacactcct gttatgggtg ctgctgctct gggttccagg ttccactggt 60  
 gacgtcaggc gagggccccc gagcctgcgg ggcagggaag ogccagcccc cagccctgac 120  
 gtcccgcccg agtgcttoga cctgctgggc cgccactgag tggcctgcgg gctcctgcgc 180  
 acgcgcgggc cgaaaacggc cggggccagc agccctgcgc ccaggacggc gotgcagccg 240  
 caggagtcgg tgggcgcggg ggcgcgcgag ggcggcggtg acaaaactca cacatgccca 300  
 ccgtgcccag cacctgaact cctgggggga cgtcagtc tctctctccc cccaaaaccc 360  
 aaggacaccc tcattgatctc ccggaccctc gaggtcacat gcgtggtggt ggacgtgagc 420  
 cacgaagacc ctgaggtcaa gttcaactgg tacgtggagc gcgtggaggt gcataatgcc 480  
 aagacaaaag cgcggggagg gacgtacaac agcacgtacc gtgtggtcag cgtcctcacc 540  
 gtctgcacc aggactgggt gaatggcaag gactacaagt gcaaggtctc caacaaagcc 600  
 ctcccagccc ccattcgagaa aacctctcc aaagccaaag ggcagccccg agaaccacag 660  
 gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 720  
 ctggtcaaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 780

```

gagaacaact acaagaccac gcctcccggtg ttggactccg acggctcctt cttctcttac      840
agcaagctca ccgtgggacaa gagcaggtgg cagcagggga acgtttcttc atgctccgtg      900
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tcccgggaaa      960
tga                                                                           963

```

```

<210> 50
<211> 320
<212> PRT
<213> Homo sapiens

```

```

<400> 50

```

```

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1          5          10          15

```

```

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
          20          25          30

```

```

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
          35          40          45

```

```

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
          50          55          60

```

```

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65          70          75          80

```

```

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
          85          90          95

```

```

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
          100          105          110

```

```

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
          115          120          125

```

```

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
          130          135          140

```

```

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
          145          150          155          160

```

```

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

```

165

170

175

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 180 185 190

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
 195 200 205

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 210 215 220

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
 225 230 235 240

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 245 250 255

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 260 265 270

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 275 280 285

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 290 295 300

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 305 310 315 320

<210> 51

<211> 107

<212> PRT

<213> Homo sapiens

<400> 51

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
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Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
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Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
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Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
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Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
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<400> 52

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Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile  
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Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
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Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln  
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<211> 119

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<213> Homo sapiens

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Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
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Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr  
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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
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Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
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Thr Leu Val Thr Val Ser Ser  
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&lt;210&gt; 54

&lt;211&gt; 119

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 54

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Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr  
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Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
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Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr  
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Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys  
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Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly  
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Thr Leu Val Thr Val Ser Ala  
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35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala  
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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
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Phe Asn Arg Gly Glu Cys  
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<213> Homo sapiens

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Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
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Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr  
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Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
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Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
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 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
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345

350

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